OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.3
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Run on: October 19, 2002, 07:56:52 ; Search time 48 seconds
(without alignments)
2343.753 Million cell updates/sec

Title:
Perfect score: 2359
Sequence: 1 MAPSDSVGDVTKTLLAASES...........DPSKALIRKVSTEADNLLEK 458

Scoring table: BLOSUM62
Xgapop 10.0 ; Xgapext 0.5
Ygapop 10.0 ; Ygapext 0.5
Fgapop 6.0 ; Fgapext 7.0
Delop 6.0 ; Delext 7.0

Searched: 383533 seqs, 122816752 residues
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Total number of hits satisfying chosen parameters: 767066

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH-0.1 -LOOPCL=0
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	827.5	35.1	1962	1	US-07-803-636A-1	Sequence 1, Appli
2	826.5	35.0	1990	6	5171685-5	Patent No. 5171685
3	826.5	35.0	1990	6	5518916-5	Patent No. 5518916
4	120	5.1	3883	1	US-08-468-036-33	Sequence 33, Appli
5	120	5.1	3883	2	US-08-376-843-33	Sequence 33, Appli
6	120	5.1	3884	2	US-09-541-782-3	Sequence 3, Appli
7	119.5	5.1	4766	5	PCT-US93-07261-10	Sequence 10, Appli
8	111	4.7	3278	1	US-08-484-105-13	Sequence 13, Appl
9	111	4.7	3278	1	US-08-484-106-13	Sequence 13, Appl
10	108.5	4.6	7568	2	US-08-694-869-2	Sequence 2, Appli
11	108.5	4.6	7568	3	US-08-349-546-2	Sequence 2, Appli
12	105.5	4.5	1766	2	US-08-453-848-8	Sequence 8, Appli
13	105.5	4.5	1766	4	US-09-169-027-8	Sequence 8, Appli
14	104.5	4.4	4071	4	US-09-091-117-3	Sequence 3, Appli
15	103.5	4.4	1407	3	US-08-688-988-7	Sequence 7, Appli
16	101.5	4.3	2134	2	US-09-799-138-3	Sequence 3, Appli
17	101.5	4.3	2134	2	US-09-392-362-3	Sequence 3, Appli
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25	99	4.2	7100	2	US-08-743-637B-169	Sequence 169, App
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27	98.5	4.2	2007	4	US-08-526-840B-169	Sequence 169, Appl
28	97.5	4.1	1829	5	US-08-688-988-9	Sequence 9, Appli
29	97.5	4.1	3279	5	PCT-US93-03077-2	Sequence 2, Appl
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34	97	4.1	3123	1	US-09-094-889-2	Sequence 2, Appli
35	96.5	4.1	912	1	PCT-US94-01149-31	Sequence 31, Appl
36	96.5	4.1	2612	5	US-08-471-033-31	Sequence 31, Appl
37	96.5	4.1	2612	1	US-08-471-044-31	Sequence 31, Appl
38	96.5	4.1	2612	1	US-08-463-483A-31	Sequence 31, Appl
39	96.5	4.1	2612	1	US-08-471-046A-31	Sequence 31, Appl
40	96.5	4.1	2612	2	US-08-470-566B-31	Sequence 31, Appli
41	96.5	4.1	2612	2	US-08-838-219B-3	Sequence 31, Appli
42	96.5	4.1	2612	2	US-08-469-334-31	Sequence 31, Appl
43	96.5	4.1	2612	3	US-09-300-529-31	Sequence 31, Appl
44	96.5	4.1	2612	3	US-09-233-336A-3	Sequence 31, Appl
45	96.5	4.1	2612	3	US-09-233-752A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-07-803-636A-1
Sequence 1, Application US/0780363A
Patent No. 5422428

GENERAL INFORMATION:
APPLICANT: McGUIRE, TRAVIS C., TERRY F. McELWAIN, LANCE E. PERRYMAN,
APPLICANT: WILLIAM C. DAVIS
TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING
TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BABESIA BIGEMINA AND SIMILAR
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 2.
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 NW 41ST STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FLORIDA
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,636A
FILING DATE: 19911206
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: WA4-059.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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LENGTH: 1962 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: NO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: BABESIA BIGEMINA
STRAIN: JG-29
INDIVIDUAL ISOLATE: MEXICO
CELL TYPE: MEROZOITE
IMMEDIATE SOURCE:
CLONE: pBbg58
FEATURE:
NAME/KEY: CDS
LOCATION: 186..1628
FEATURE:
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LOCATION: 186..248
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LOCATION: 1884..1889

US-09-807-459-2
US-07-803-636a-1
DB:

Alignment Scores:
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Score:                  827.50
Percent Similarity:     59.12%
Percent Identity:       41.80%
Best Local Similarity:  35.08%
Query Match:
DB:                     1

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Conservative:  75
Mismatches:    140
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US-09-807-459-2 (1-458), x US-07-803-636A-1 (1-1962)

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Qy   44 AsnPheAlaGluArgIleCysSerSerGlnIleValProLysGlySerAsnCysSerSerAlaSerVal  63
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Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla  103
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Db  516 -------AAGTACAAGCCCGTTGAGTCTCCAAAATCCTTACCAGTTGACGCGTGC  563

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Qy  124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu  143
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Db  738 TTCTACACATTGACTACGTTGTACTACAAGACTTACCTGACCTTACGGCGGCCTAAG  797

Qy  184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaAlaLeu  203
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Qy  244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuLeuAlaThrValAlaGly  263
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Qy  264 TyrValAspThrProTrpTyrLysLysTyrMetGlyLeuLysLysAspPheMetValAsn  283
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Db 1212 AGCACCAAAGCATATTGCCAAC--GGTGTACGTGATTTGTCAAGGATGAATTAAGGAG---  1265
Qy  343 ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle------------Gly  356
           |||   :::||||||||||||||||||||||:::         Gly
Db 1266 --CCTAGCCAACAAATAATTCGTGAGAAGCTGCCTCACTACCTTTCTAAGGCA  1316
Qy  357 GlnGlyThrValAspPhePheAsnLysGluIleLeuArgAsp------ProSerLysAlaLeu  374
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Db 1371 ---CAAAAGGGGCGACCACCATCCGAAGCAGCTGTAGAGGAAAACCGTTCCGTCTGGC---  1424
Qy  395 ValAspPheIleAsnAsnGluIleLeuArgAspProSerLysAlaLeuIleLeuArgLysValTyr  414
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Qy  415 Thr------                                         GluAlaAspAsp  419
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Pred. No.:             1.9e-92
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Best Local Similarity: 35.53%
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DB:

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Qy   61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnLeuThrLeuGlnSer   80
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Db  392 GAGGTAGTTACAGAATTATGCTGACCGTTGTGAAATGTACGGATGCTTTACGATTGACAAT   451

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Db  452 GTCAAAATATCCGTTGTGATCAAGAGTACCAAACCTCTATCTCTTCCAAACCCTTACCAGTTG   511

Qy  101 GluLeuAlaAlaPheIleLeuPheLysGlySerAspAlaAsnProAlaAsnSerThrGlyLys   120
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Db  512 GATGTCCGTTCAGATATTGTTCAAAAGAGAGTCGCATCGAACCCTGCCAAGAACAGCGTAAA   571

Qy  121 ArgPheThrArgMetArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe   140
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Qy  141 AsnLeuLeuGluLysAsnValThrArgAspAlaAlaAspThrIleGluAsnPheAla   160
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Db  632 GGTCTGTTGAACAACAATGTTGTGCACCAGGAAGGAACTACCGATGTTGAATATCTTGTC   691

Qy  161 SerArgTyrLeuThrMetAlaThrLeuThrTyrTyrLysThrTyrThrAsnValAspGluPhe   180
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Db  692 AACAAGTACTCTCTATATGGCTACCCATGAAACTACAGAACTTATTTGACAGTAACAGTATG   751

Qy  181 GlyAlaSerPhePheAsnLysLeuSerPheThrHisGlyLeuPheGlyIleTyrIleLys   200
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Db  752 AACGCCAAGTCTCTTCAACAGATTCAGTCACTCACTAACAAATATTCAGTCGTCGTATTAGG   811

Qy  201 ArgAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSer   220
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Db  812 CAAACATTGAGTGAATATCATCAGGTGGAATGTTCCTGAAGATTTT---GAAGAAAGGAGC   868

Qy  221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspThrGlnIleIlePro   240
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Db  869 ATCGAAACGTATCACTCAACTTACTACGCAGAAGATTACATGTTGACCCAGATTCCA   928

Qy  241 AlaLeuProLysSerArgPheSerLeuMetValValGlnArgLeuLeuAlaThr   260
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Qy  261 ValAlaGlyTyrValAspThrProThrProThrTyrTyrMetLysLeuLysAsnPhe   280
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Qy  281 MetValAsnArgValPheIleProThrHisLysLysPhe   292
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Qy  293 ------PheAsnLysGluIleArgGluProSerLysAlaLeuLysGlu   306
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Qy  307 LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnThrValAsp   326
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Db 1229 GAGGCTCCTCAAGTCACCAAAACACTTCTTCGATGAGAACATTGGCCAACCACCAAGGAG   1288
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Qy  327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAsp   346
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Db 1349 ACCAAGGAGTTCTTC--AGGGAGGCTCCTCAAGTCACCAAGCACTCTTCCTAGGCGGAGAAT   1405

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Qy  387 GluAsnLysIleGluGlyGlnGlyThrValAspPhe-------------------   397
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Qy  398 ------IleAsnAsnGluIleArgAspProSerLysAlaLeuLeuArgLysValTyrThr   415
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Db 1586 GGCGCCAAGAAT---TTCATTTCCCAGCCCATGAAGGTACTAACGAAGTTCTTAAACGAA   1642

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Qy  455 Leu   455
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Db 1703 TTA   1705
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RESULT 3
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;Patent No. 5518916
;APPLICANT: MCELWAIN, TERRY F.;MCGUIRE, TRAVIS C.;JASMER,
;DOUGLAS P.;REDUKER, DAVID W.;GOFF, WILL L.;STILLNER, DAVID
;TITLE OF INVENTION: CLONED BABESIA DNA
;NUMBER OF SEQUENCES: 7
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/342,480
;FILING DATE: 21-NOV-1994
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 989,616
;FILING DATE: 14-DEC-1992
;APPLICATION NUMBER: 504,461
;FILING DATE: 04-APR-1990
;APPLICATION NUMBER: 333,155
;FILING DATE: 04-APR-1989
;SEQ ID NO:5:
;LENGTH: 1990
5518916-5
LENGTH: 1990

Alignment Scores:

Pred. No.:	1.9e-92	Length: 1990
Score:	826.50	Matches: 178
Percent Similarity:	51.30%	Conservative: 79
Best Local Similarity:	35.53%	Mismatches: 195
Query Match:	35.04%	Indels: 49
DB:	6	Gaps: 6

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US-09-807-459-2 (1-458) x 5518916-5 (1-1990)

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Qy  21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla   40
       :::   |||
Db 272 ATGACTCTCCGTGACCACATGCACAACATTACTAAGGATATGAACACAGTTTTGAGCAAT   331

Qy  41 ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer   60
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Db   332 GGTCGTGGAGCAGATTGTAAATGATGTTTGCTCTAAAGCTCCTGAGGACTCCAAACTCGT          391
            ::: |||||||                ||||||      :::|||:::
Qy    61 AlaSerValSerAlaThrTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer                80
            |||||:|      ||:|                                |||::::|
Db   392 GAGGTAGTTAACAAATTATCGTCACGCGTTGTGAAAATGTACGGATGCTTTACGATTGACAAT          451

Qy    81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu                100
            :::||||||||||             :::::||||||||:::||||::::||||||||||
Db   452 GTCAAAATATCGTTGTATCAAAGTACCAACCTCTATCTCTTCCAAACCCTTACCAGTTG          511

Qy   101 GluAlaAlaAlaPheIleLeuPheLysGlySerAspAlaAsnProAlaAsnSerThrGlyLys                120
            |||    |||:::|||||:::|||:::||||||:::||||||||||||:::::
Db   512 GATGCTGCGTTCAGATTGTTCAAAGGAAGTCCATCCAAACCCTGCCAAGAACAGCCGTAAAA          571

Qy   121 ArgPheTrpMetArgPheAspArgArgGlyLysAsnHisSerThrTyrPheHisAspLeuValPhe                140
            |||||||      ||| ||||||                  |||              |||
Db   572 CGCGAAATGGTTCGCGTTTCAGAAATGGAGCGAAACCATTGGTTGAATATCTTCGTCACT          631

Qy   141 AsnLeuLeuGlyLysAsnValThrArgAspAlaAlaThrArgAspIleGlnAsnPheAla                160
            ||||||       :::|||                |||:::||:::||||::|||
Db   632 GGCTCTGTTGAACAACAATGTTGTGCACGACGGAAGAAACTACCACGGATGTTGAAAATATCTCACT          691

Qy   161 SerArgTyrTyrLeuTyrMetAlaThrLeuThrLeuTyrTyrTyrThrArgAsnValAspGluPhe                180
            ||:        |||  ||::::||::::                   |||:::|||
Db   692 AACAAGGTACTCTATATGGCTACCATGAACACTTATTTGACAGTAAACAGTATG          751

Qy   181 GlyValAlaSerPheProAsnLysLeuSerPheTheThrThrGlyLeuPheGlyTrpGlyIleLys                200
            ||      ||||||                |||:::||:::||::::
Db   752 AACCCAAGTGTTCTTCAAACAGATTCAGCTTCACTACAAAGATATTCAGTCGTCGTATTAGG          811

Qy   201 ArgGlyAlaLeuHisGlyIleIleLeuArgSerAsnLeuProLeuIleGlyLysThrGluHisSer                220
            |||  |||||                        :::||||||:::
Db   812 CAAACATTGAGTGATATCATCAGGTCGAATGTTCCTGAAGAATTT--GAAGAAGGAGC          868

Qy   221 ValSerArgLeuGlnHisIleThrSerSerTyrGlyLysProThrArgGlnIlePro                240
            |||              :::||||||
Db   869 ATCGAACGTATCACTCAACTTACTACCACGTACGAAGATTCATCA          928

Qy   241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnAsnArgLeuLeuAlaThr                260
            ||| |||      ||||||   ::::                |||:::
Db   929 ACTCTTTTCCAAGTTTGCCACGTCGTTATGTCTGAAGGTGAAGAAGGTTCTTGCTCGGTAGC          988

Qy   261 ValAlaGlyThrTyrValAspThrProProThrProTyrTyrMetLysLeuLysAsnPhe                280
            |||        |||:::::               ||:::||||||:::
Db   989 TTGACCTCGTACGTTTGGTACAAAGATGGAAACATATTCAGGAGACTTT          1048

Qy   281 MetValAsnArgValPheIleProThrThrLysLysPhe---------                292
            |||
Db  1049 TTCTCTAAAAACGTTACCCAACCTACAAAAGAAGTTCATCGAGGAAGTTACC          1108

Qy   292 ----------                                                  292
Db  1109 AAAAACTATCTGAAAGCCAATGTTCCTGACCCCACTAAAAAGTTTATGCAGGAACACTCAC          1168

Qy   293 ----------PheAsnLysGlyIleArgGluProSerLysAlaLeuLysGlu                306
                      |||:::
Db  1169 GAAAAACCAAAGGCTATCTGAAAGAGAATGTAGCCGAAACCTACTAGACTTTTTTCAG          1228

Qy   307 LysValSerThrAspThrLysSerAspLeuAsnLysLysGlyIleGlnGlyThrValAspAsp                326
            |||||                     ||::::||| :::
Db  1229 GAGGCTCCTCAAGTCACCAAAACACTTCTTCGATGAGAACATTGGCCAACCCACCAAGGAG          1288

Qy   327 PhePheAsnLysGlyIleAsnArgAspProSerLysAlaLeuLysGluLysValSerAsnAsp                346
            |||:::||        :::|||:::
Db  1289 TTTTTCAGGAGAAGCGTTCCCAAAGCCACTAAAACATTTCCTACGACGAAAAACATCGGTCAAACCA          1348

Qy   347 AlaLysAspLeuPheGluAsnLysGlyIleGlyThrValAspPheIleAsnAsnGlu                366
            |||      ||: :::||:::|||
Db  1349 ACCAAGGAGTTCTTC---AGGGAGGCTCCTCAAGCCACTAAGGCCACTTCCTAGGCGGAAT          1405

Qy   367 IleArgAspProSerLysValAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPhe                386
            |||:::|||    ||||::|||
Db  1406 ATTGCTCAACCTACTAAAGAATTTTCAAGGATGTCCCTCAAGTCACCAAGAAGGTTATA          1465
```

```
Db  1406 ATTGCTCAACCTACTAAAGAATTTTCAAGGATGTCCCTCAAGTCACCAAGAAGGTTATA          1465

Qy   387 GluAsnLysIleGlyGlnGlyThrValAspPhe-------------------------                397
            |||
Db  1466 ACTGAGAACATTCCTCAACCACTAAGGAGTTCCGGAGGTTCTCATGCTACCATG          1525

Qy   398 ------IleAsnAsnGluIleArgAspProSerLysAlaLeuIleLeuArgLysValTyrThr                415
              :::|||                   |||:::|||      ||||::|||
Db  1526 AAAGTCTTGAATGAAAAACATTGCTCAACCTGCCAAGAAAATCATTACAGAGTTTGGTACA          1585

Qy   416 GlyAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe                435
            |||      ::::||:::|||
Db  1586 GGCGCCAAGAAT--TTCATTTCCGCAGCCCATGAAGGTACTAAGCAGTTCTTAAAGGAA          1642

Qy   436 GluIleArgAspProSerLysAlaLeuIleLeuArg---LysValSerThrGluAlaAspAsn                454
            ::: |||                ||||::|||     ::: ||| ::::
Db  1643 ACTGTTCGGCCAACCTACAAAGAGAATTCCTGACGAGCTTTGAAAACTACTAAAGACGCCA          1702

Qy   455 Leu                455
            |||
Db  1703 TTA          1705
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Query Match: 5.09%
DB: 1

Indels: 186
Gaps: 29

US-09-807-459-2 (1-458) x US-08-468-036-33 (1-3883)

Qy   4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
           ||||||||:::: |||||| ||||||||:::
Db   1051 AGGGATGCACCAGGAATTATACCGAGGGTTCTTTGAAGTTGGTTTGACACATTGGAACTA 1110

Qy   24 AlaAlaAlaAsnAlaTyrMetIle------------AsnSerAspMetSer 35
           |||::: |::::
Db   1111 CAACAGAAACGATTACCTAGTAAAAATGTTCGTTCATTGAACTCTACAACGAGAAATTGAAG 1170

Qy   36 AspTyrLeuSerAlaAlaValSerAsp----------AsnPheAla 46
           ||||| |||::: |||
Db   1171 GACCCTCTTGGACAGCAGAATACCAACGCGGCTCTCAGTAATATACTGGCTTTGACGCGCCAATTTATG 1230

Qy   47 GluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerValAlaTyr 66
           ||||||| |||::: |::|| |::||
Db   1231 AAAAAAATTGAGGATTTTGCTTCAAGCACGACAGCAAATAATACCACTAGCACAGTGCTAGT 1290

Qy   67 MetSerArgCysAlaLysGlnAspCys----------LeuThrLeuGln 79
           ||||||| |||||| :::
Db   1291 AGTTCCAGGAGTAATTCTAGGAACAGTTCTCCGAGGTCATTAAATGATCTAACACTTAAA 1350

Qy   80 Ser---------LeuLysTyrProLeuGlyLysTyrGlnProLeuThrLeuProAspPro 97
           ::: |::|| |||:::
Db   1351 GCTCGTCTTATTAAGAAAAAGGTTAAGGACAAAAATCACTGCCGAATACCATTAAGCAACAG 1410

Qy   98 TyrGlnLeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProLeuAsnSer 117
           |||||| :::|| |::||
Db   1411 TATCAACACAACAGGCAGGTGAATTCCAGGAACAACACTCTTCCTCTAACTCTGGCTCTACC 1470

Qy   118 ThrGlu-----------------------LysArgPheTrpMetArgPhe 126
           ||| |||
Db   1471 ACTAATAATGCTTCTAGTAACCACACAAATAACGGTCAAAGAAGTTCGGATTGGATGCGTCCA 1530

Qy   127 ArgArgGlyLysAsnHisSerTyrPheHisAspLeuVal------------- 139
           ||| |::||
Db   1531 AATGACCAAACTAATGGTATATACATCCCAGAATTTCCAAGAATTTCACATAACAAAATGCT 1590

Qy   140 -----------------PheAsnLeuGluLysAspValThr---ArgAspAlaAspThrAsp 155
                            ||||||||:::: |||
Db   1591 ATGGAGGGGGCTAAACCTATTACAAAAAGGCTTAAACCATAGGCAAGTAGCGTCCCACTAAA 1650

Qy   156 IleGluAsnPheAlaSerArg--------TyrLeuTyrMetAlaThrLeuTyrTyrLysThr 173
           ::::|| ||||||| |||||||||
Db   1651 ATGAACGATTTTTCCAGTAGATCTCATACCAATTTTTACAATCACTTTGTATAAGAGCAT 1710

Qy   174 Tyr------------------------------ThrAsn 176
           ||| |||
Db   1711 CAGGATGAACTATTTAGAATTTCCAAAAAATGAAATCTTGTGAATTACTGGTTCAGAAAAC 1770

Qy   177 ValAspGluProPheGly--------------AlaSerPhePheAsnLysLeu 188
           ||| |||
Db   1771 ATCAACAGAATCCGGAGCCATTAAATCAACGTCCAAAGAGCTGGTTCAATCAACAAAGT 1830

Qy   189 SerPheThrThrGly------------ 193
           |||
Db   1831 CTATTGACGCTGGGCAGGGTCATAAACGCACTCGTAGATAAAACGGGCCATATACCTTTC 1890

Qy   194 --------------LeuPheGlyTrpGlyIleLysArgGln 202
                         ||| |||
Db   1891 CGTGAATCGAAATTGACCCGCCCCTGCTTCAGAGATTCCCTGGGGTTGGTTAATAACGGCA 1950

Qy   203 LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyTyrThrGlnHisSerValSer 222
           |::|: ||||:::: |||:::
Db   1951 CTA----ATTGCTACTATATCGCCTCCAAAGGTAACTCTCGAAGAAAACCTGCAGT 2001

Qy   223 ArgLeuGlnHisIleIleArgThrSerSerTyrLysAspTyrMetAspThrGlnIleProAlaLeu 242
           |::::: ||||::::
Db   2002 ACATTAGAGTAT---GCTTCGAAGGGCTAAAAAACATTAAGAACAAG-----CCGCAACTG 2052

Qy   243 ProLysPheAlaLysArgPheSerLeuMet--------------------Val 253
           ||| |:::
Db   2053 GGTTCATTTATAATGAAGGATAATATTTTGGTTAAAAATATAACTAATGGAATTGCAAAGAATT 2112

Qy   254 ValGlnArgLeuLeuAlaThrValAlaGly-------TyrValAspThrProTrpTyr 270
           ||||||| |::|| |||
Db   2113 AAATCCGATTTACTCTCTCACAAAGTCCAAAGAAGGAAGAAATATATGAGGCAAGATCACTAC 2172

Qy   271 LysLysThrLysTyrPheMetLysLysLeuLysAsnPheMetValAsnArgValPheIleProThrLys 290
           |||||| |||::: |::|| |||
Db   2173 AAAAAATTGAACAGTGATTTAGAAAAGTTATAAA--AATGAAGTT-- 2214

Qy   291 LysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLeuLysAspGluLysSerThr 310
           ||| |:::|| |||
Db   2215 --------CAAGAAGTAAAAAGATGGAAAATTGAAAGTTTGACATCGAAAAAAGCATTG 2262

Qy   311 AspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhePheAsnLys 330
           |||||||:::: |::|| |||
Db   2263 CTAGTAAAAAAGATAAAAATGAAGTCAAAA----GAAACTAAATTCAATCTCAAAATTGC 2313

Qy   331 GluIleArgAspProSerLysAlaLeu------------------LysGlu 341
           |::|| |::||
Db   2314 CAAATAGAATTCATTGAAAACTACCATAGATCATTTAAGGGCACAAACTAGATAAAACAGCAT 2373

Qy   342 LysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr------- 359
           ||| |::|| |||
Db   2374 AAAACTGAAATTGAAATTATCCGAT---TTTAATACAACAACTACAGAAGGTTGACTGAAGTA 2430

Qy   360 ------------------------------ValAspPhe 362
                                         |||
Db   2431 ATGCAAAATGGGCCCTACACGTGATTACAAAAAAGAGGACAACTTAATCAAAAGTTTGAA 2490

Qy   363 IleAsnAsnGluIleArgAspProSerLysAlaLeuLeuLeuLysAspGluLysSerThr 380
           ::: |||||:::: |||
Db   2491 ATGGCATAATTACTAAAGAAATTGAAATCTCACGTGTTTTTACAAATTAAACACT 2550

Qy   381 GlyAlaGluAsp-----LeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle 398
           :::|| |::|| |||
Db   2551 ATCGACAACAGGAAAGTAGTATTCTTCAAGAGACTAAATAATC---CAACCAAAATCTTGATATGATC 2607

Qy   399 AsnAsnGluIleArgAspProSerLysAlaLeu----------------------- 409
           |||||::: |||
Db   2608 AAAAATGAAGTACTGACTCTTATGAGAACCATCCAAGAAAAAGCTGACTAATGTACAA 2667

Qy   410 -----IleArgLysValTyrThrGluLeuAlaAspLeuPheGlu-------AsnLys 424
                ||| |::|| |||
Db   2668 GACTGTGTGAAGAAAAATTTTAAACGAATCCTAAATTCTCAATGTTGTTATTGTAGAGAA 2727

Qy   425 IleGlyGlnGlyThrValAspPhe-----IleAsnLysGluArgAspProSerLys 442
           ||| |::||
Db   2728 ATCGACATAATAAGGAGTAGAATTCCAAAATTTTATAAAAAAAGAGATTAAGCCGAGAT----- 2781

Qy   443 AlaLeuIleArgLysValSerThrGluAlaAspAsnLeu 455
           |::: ||| |||
Db   2782 -----CTTTCTGATATTAGGCGAAGAAAAATAACAACATG 2814

RESULT 5
US-08-376-843-33
Sequence 33, Application US/0837684
Patent No. 5846764

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COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/376,843
  FILING DATE:
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/184,605
  FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
  NAME: No. 584676serland, Greta E.
  REGISTRATION NUMBER: 35,302
  REFERENCE/DOCKET NUMBER: 27866/31784
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312/474-6300
  TELEFAX: 312/474-0448
  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3883 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)

US-08-376-843-33

Alignment Scores:
  Pred. No.:                   0.000286
  Score:                       120.00
  Percent Similarity:          34.75%
  Best Local Similarity:       19.74%
  Query Match:                 5.09%
  DB:                          2

  Length:        3883
  Matches:        121
  Conservative:    92
  Mismatches:     214
  Indels:         186
  Gaps:            29

US-09-807-459-2 (1-458) x US-08-376-843-33 (1-3883)
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Qy    4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer   23
        |||||||||| |||:::
Db 1051 AGCCATGCAGCCAGGAGAATATACCGGAGGGTTCTTTGAAGTTGTTGTTGACACATTGGAACTA 1110

Qy   24 AlaAlaAsnAlaTyrMetIle------------------------AsnSerAspMetSer   35
        ||| ||||||||||            :::|||
Db 1111 CAACAGAACGATTACGTACGTAGTAAAANTGTTCGTTCANTTGAACTCTCTACACGAAGAANTTGAAG 1170

Qy   36 AspTyrLeuSerAlaLeuSerAsp-------------------AsnPheAla   46
        ||| ||  |||:|::         |||
Db 1171 GACCCTCTTGGACAGGCAATAGCAACGGCTCTAGTAATACTGGCTTTGACGGCCAATTATG 1230

Qy   47 GluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyr   66
        ::||||||:::|||                |||:|||
Db 1231 AAAAAATTGAGGATTTTTGCTTCAAGCACAGCAAATAATAACCTAGCAACAGAGTGCCTAGT 1290

Qy   67 MetSerArgCysAlaLysGlnAspCys----------------LeuThrLeuGln   79
        |||                          :::  ||||  :::
Db 1291 AGTTCCAGGAGTAATTCTAGGAACAGTTCTTCCGAGGTCATTAAANTGATCTAACACCTAAA 1350

Qy   80 Ser------LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspPro   97
        :::      |||                |||        |||
Db 1351 GCTGCGTCTATTAAGAAAAAGGTTAAGGACAAAATCACTGCCGAATACCATCAAGCAACAG 1410

Qy   98 TyrGlnLeuGluAlaLeuAlaPheIleLeuPheLysGluAspSerAlaAsnProAlaAsnSer  117
        |||||||        |||                 :::|||
Db 1411 TATCAACAACAGGCAGTGAATTCCAGGAACAACTCTTCCTCTAACTGTCTGGCTTCCTACC 1470

Qy  118 ThrGlu---------------LysArgPhetrpmetArgphe  126
        |||                   |||
Db 1471 ACTAATAATGCTTCTTAGTAACACACCAAATAACGGTTCAAAATGAGAGAAGTTCGATGGCTCCA 1530

Qy  127 ArgArgGlyLysAsnHisSerTyrPheHisAspLeuVal------------------  139
        |||                   |||                   ::||
```

```
Db 1531 AATGACCAAAACTAATGGTATACATCCAGAATTTGCAAGGAATTTCACATAACAAATGCT 1590
Qy  140 ------PheAsnLeuLeuGluLysAsnValThr---ArgAspAlaAlaProAlaThrAsp  155
        |||       :::  |||                |||
Db 1591 ATGGGAGGGCGGCTAAACCTTATTACAAAGGCTTAAACGCATAGCGAAGCCGTCCACTAAA 1650

Qy  156 IleGluAsnPheAlaSerArg------TyrLeuTyrMetAlaThrLeuTyrTyrLysThr  173
        ::: |||:::||||:||||||          |||
Db 1651 ATGAACGAGTTTTTCCAGTAGATCTCATCACTTTTACATACTTTGTATAAGAAGCAT 1710

Qy  174 Tyr------------------------------------ThrAsn  176
        |||                                    |||
Db 1711 CAGGAGGAAACTATTTAGAAATTTCCAAAATGAATCTTCTGGATTTAGCTGAGAAAC 1770

Qy  177 ValAspGluPheGly------------AlaSerPheAsnLysLeu  188
        |||                        |||:::
Db 1771 ATCAACAGATCCGGAGCATTAAATCAACGTGCCAAAAGAAGCTGGTTCAAATCAACCAAAGT 1830

Qy  189 SerPheThrThrGly--------------------  193
        |||                            |||
Db 1831 CTATTGACGCGTCGGGCAGGGTCATACAAACGCACTCGTAGATAAAAGCGGCCCATATACCTTC 1890

Qy  194 ------LeuPheGlyTrpGlyIleLeuLysArgAla  202
        |||   |||                |||
Db 1891 CGTGAATCGAAATTGACCCGCCGCTTCAAGAGTTCCCTGGGTGGGTAATACGAAAAACCGCA 1950

Qy  203 LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyLysThrGluHisSerValSer  222
        |||                   |||                        :::|||
Db 1951 CTA------ATTTGCTACTATATATCGCCTGCAAAGGTAACTTCTGAAGAAAACCTGCAGT 2001

Qy  243 ProLysPheAlaLysArgPheSerLeuMet------------------------Val  253
        |||                       |||                            |||
Db 2002 ACATTAGAGTAT---GCTTCGAAGGCTAAAAAACACATTAAGAACAAG-----CCGCAACTG 2052

Qy  223 ArgLeuGlnHisIleIleThrSerSerTyrTyrMetAspThrGlnIleProAlaLeu  242
        |||||:::|||                   :::|||
Db 2053 GGTTCATTTATPATGTAAGGGATANTTTGGTTAAAAATATAACTTATGGAATTAGCAAGATT 2112

Qy  254 ValGlnArgLeuLeuAlaThrValAlaGly---------------TyrValAspThrProTrpTyr  270
        |||:::|||                                   |||:::
Db 2113 AAATCCGATTTACTCTCTACAAAGTCCAAAGAGGAATATATATGGACCCAAGATCACTAC 2172

Qy  271 LysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgValPheIleProThrLys  290
        |||               :::||||||||
Db 2173 AAAAAATTTGAACAGTGATTTAGAAAAGTTTATAAA---AATGAAGTT--- 2214

Qy  291 LysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSerThr  310
        :::|||                   |||||            :::
Db 2215 ------CAAGAATGTAAAAGAGAAAATTGAAGTTTGCACATGGAAAAATGCATTG 2262

Qy  311 AspThrThrLysAspLeuPheGluAsnLysIleIleGlyIleGlyThrValAspPhePheAsnLys  330
        |||||||        |||                :::|||
Db 2263 CTAGTAAAAGATAAATTGAAGTCAAAA------GAAACTATTCAATCTCAAAATTGC 2313

Qy  331 GluIleArgAspProSerLysAlaLeu---------------LysGlu  341
        |||                           |||                :::
Db 2314 CAAATAGAATCATTGAAAAACTACCATAGATCANTTAAGGGACAACTAGAATAAACAGCAT 2373

Qy  342 LysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleIleGlyIleGlyThr------  359
        |||||:::        |||||||:::  |||
Db 2374 AAAAACTGAAATGAAAATATCCGAT---TTTAATAACAAACTACAGAAGTTGACTGAGGTA 2430

Qy  360 ------ValAspPhe---------------  362
        |||   |||                  |||
Db 2431 ATGCAAAATGGCCTACATGATTACAAAAAAAGAGAACTTGACCTTAATCAAAAGTTTGAA 2490

Qy  363 ------IleAsnAsnGluIleargAspProSerLysAlaLeuIleArgGlyLysValSerThr  380
        |||   :::||||||||                        |||:::
Db 2491 ATGCATATTACTAAAGAAATTAAAAATTGAAATCTACACGTGTTTTTTACAATTAAAACACT 2550

Qy  381 GlyIleAlaGluAsp------------LeuPheGluAsnLysIleGlyIleGlyThrValAspPheIle  398
        :::||||||:::  |||          :::|||
Db 2551 ATGCAACGAGGAAAAGTATTCTTCAAGAAGACTAATATC---CAACCAAAATCTTGATATGATC 2607
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RESULT 6

US-09-541-782-3

Sequence 3, Application US/09541782

Patent No. 6284480

GENERAL INFORMATION:

APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe

TITLE OF INVENTION: Antifungal Assay

FILE REFERENCE: 1015

CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 3
LENGTH: 3884
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae

US-09-541-782-3

Alignment Scores:

Pred. No.:

Score	120.00
Percent Similarity:	34.75%
Percent Identity:	19.74%
Query Match:	5.09%
Best Local Similarity:	4

SOFTWARE: FastSEQ for Windows Version 4.0

DB: US-09-807-459-2 (1-458) x US-09-541-782-3 (1-3884)

Length:	3884	
Matches:	121	
Conservative:	92	
Mismatches:	214	
Indels:	186	
Gaps:	29	

Qy   399 AsnAsnGluIleArgAspProSerLysAlaLeu--------------------------------- 409
           ||||||||::   ::
Db   2608 AAAAATGAGTACTGACTCTTATGAGAAGCTGAACTAATGTACAAA 2667

Qy   410 -----IleArgLysValTyrThrGluAlaAspLeuPheGlu------------------ AsnLys 424
                  ||||::   ::::|: |||
Db   2668 GACTGTGTGAAGAAAATTTAAACGGATCCTCTAAATTCTTCAAGTTGTTATTGAGAAA 2727

Qy   425 IleGlyGlnGlyThrValAspPhe------IleAsnLysGluIleArgAspProSerLys 442
           ||||:|||||||||||| ||| :::
Db   2728 ATCGACATAATAAGAGTAGATTTCCAAAAATTTATAAAAATATAGGCGAGAAT------ 2781

Qy   443 AlaLeuIleArgLysValSerThrGluAlaAspAsnLeu 455
           :::: ||||||| ::::|||:||
Db   2782 -----CTTTCTGATATTACCGAAGAAAAATAACACATG 2814

Db   1412 TATCAACAACAACAGGCAGTGAATTCCAGGAACAACTCTTCCTCTAACTCTGGCTCTACC 1471

Qy   118 ThrGlu-- LysArgPheTrpMetArgPhe 126
           :::||| ||::|||
Db   1472 ACTAATAATGCTTCTAGTAACACCAACACAAATAACGGTTCAAAGAAGAAGTTCGATGGCTCCA 1531

Qy   127 ArgArgGlyLysAsnHisSerTyrPheHisAspLeuVal------------------- 139
           ||| |||
Db   1532 AATGACCAAACTAATGGTTATATACATCCAGAATTTGCAGAATTTCACATAACAAATGCT 1591

Qy   140 ---------PheAsnLeuLeuGluLysAsnValThr---ArgAspAlaAlaThrAsp 155
           |||||||||::|| :::||
Db   1592 ATGGAGGGGCTAAACCTAATTACAAAAAGGCTTAAAGCATAGGCAAGTAGGTCCACTAAA 1651

Qy   156 IleGluAsnPheAlaSerArg------- TyrLeuTyrMetAlaThrLeuTyrTyrLysThr 173
           ::::|||:::|||||||||||
Db   1652 ATGAACGATTTTCCAGTAGATCTCATACCAATTTTACAATCACTTTGTATTAGAAGCAT 1711

Qy   174 Tyr--------------------------------------- ThrAsn 176
           ||| |||
Db   1712 CAGGATGAACTATTTAGAGAATTCCAAAATGAATCTGTTGGGATTTAGCTGATTTCAGAAAAC 1771

Qy   177 ValAspGluPheGly---------------------- AlaSerPheAlaAsnLysLeu 188
           :::::::||| ||||||
Db   1772 ATCAACACAGATCCGGAGCAGCATTAAAATCAACGTGCCAAAAGAAGCTGGTTCAATCAACCAAAGT 1831

Qy   189 SerPheThrThrGly---------------------------------- 193
           ||| |||
Db   1832 CTATTGACGCTGGGCAGGGTCATGAAACGCCACTCGTAGAATAAAAACGCCCATATACCTTTC 1891

Qy   194 ---------------------- LeuPheGlyTrpGlyIleLeuLysArgAla 202
                                        ||| |||
Db   1892 CGTGAAATCGAAATTGACCCGCCTGCTTCAAGATTCCCTGGGTGGTGAATACGAAAAACCGCA 1951

Qy   203 LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer 222
           ||| :::: |||
Db   1952 CTA--------AATTGCTACTATATCCGCCTGCAAAAGGTAACTTCTGAAGAAAACCTGAGT 2002

Qy   223 ArgLeuGlnHisIleThrSerSerTyrLysAspThrMetAspThrGlnIleIleProHis 242
           |||::::||| :::|||
Db   2003 ACATTAGAGTAT---GCTTCGAAGGCTAAAAAACATTAAAATCAACGTGGTTCAATCAACCAAAGT 2053

Qy   243 ProLysPheAlaIleArgPheSerLeuMet------------------ Val 253
           :::||| :::
Db   2054 GGTTCATTTTATAATGAAGGATATATTTTGGTTAAAAATATAACTATGGAATTAGCAAAGAATT 2113

Qy   254 ValGlnArgLeuLeuGluAlaThrValAlaGly---------- TyrValAspThrProTrpTyr 270
           ||||| :::
Db   2114 AAATCCGATTTACTCTCTACAAAAGTCCAAAGAGAGGAAATATATATGAGCGAAGAACACTAC 2173

Qy   271 LysLysTrpIleTyrMetLysLysLeuLysAsnPheMetValAsnArgValPheIleProThrLys 290
           ||||| ||::::||| :::
Db   2174 AAAAAATTGAACAGTGATTTAGAAAGTTTATAA---AATGAAGTT---CCGCACTG 2215

Qy   291 LysPhePheAlaLysValGluArgGlyProSerLysAlaLeuLeuLysLysValSerThr 310
           ||| ::::||| :::|||
Db   2216 -----------CAAGAATGTAAAAGAGAAATTGAAAGGTTTGACATCGAAAAATGCATTG 2263

Qy   311 AspThrLysAspLeuPheGluAsnLysIleGlyThrValAspPhePheAsnLys 330
           :::||| ||||||
Db   2264 CTAGTAAAAGATAAAATTGAAGTCAAAA----- GAAACTATTCAACATCTCAAAAATTGC 2314

Qy   331 GlyIleArgAspProSerLysAlaLeu----------------------- LysGlu 341
           ||| :::|||
Db   2315 CAAATAGAATCATTGAAAACTACCATAGAATCAATAAAACAGCAT 2374

Qy   342 LysValSerAsnAspAlaLysAspPheGluAsnLysIleGlyIleGlyThr--------- 359
           |||::::||||| ||||||
Db   2375 AAACTGAAATTGAAATATCCGAT---TTTAATAACAAACTACACAAAGTTGACTGAGGTA 2431

Qy   360 -------------------- ValAspPhe----------- 362
                                      :::|||
Db   2432 ATGCAAAATGGCCCTACATGATTACACAAAAAGAGAACTTGACTTTAATCAAAAGTTTGAA 2491

Qy   4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
           ||| :::
Db   1 AGCGGATGCAGCAGGAATTATACCGAGGGTTCTTTTGAAGTTGTTTGACACATTGGAACTA 1111

Qy   24 AlaAlaAsnAlaTyrMetIle--------------------- AsnSerAspMetSer 35
           ||| |||
Db   1112 CAACAGAACCGATTACCTAGTAAAAATGTTCGTTCATTGAACTCTACAACGAGAGAATTGAAG 1171

Qy   36 AspTyrLeuSerAlaValSerAsp--------------- AsnPheAla 46
           ||| |||
Db   1172 GACCTCTTGACAGACAAATACCAACGCGCTCTAGTAATATAACTGCCTTTGACGGCCAATTTATG 1231

Qy   47 GluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerValSerA1aTyr 66
           |||::::   :::
Db   1232 AAAAAATTGAGGATTTTGCTTCAAGCACAGCAAATAATACCACTAGCAACAGTGCTAGT 1291

Qy   67 MetSerArgCysAlaLysGlnAspCys------------------ LeuThrLeuGln 79
           ||| |||||
Db   1292 AGTTCCAGGAGTAATTCTAGGAACAGTTCTCCGAGGTCATTAAATGATCTAACACCTAAA 1351

Qy   80 Ser----------- LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspPro 97
           ::: |||
Db   1352 GCTCTGCTCTTATTAAAGAAAAAGGTTAAGGACAAAAATCAACTACTGCCGAATACCATCAAGCAACAG 1411

Qy   98 TyrGlnLeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProLeuAsnSer 117
           |||||| ||| ::::|||
Db   2432 ATGCAAAATGGCCCTACATGATTACACAAAAAGAGAACTTGACTTTAATCAAAAGTTTGAA 2491

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RESULT 7
PCT-US93-07261-10
Sequence 10, Application PC/TUS9307261
GENERAL INFORMATION:
  TITLE OF INVENTION: PfEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF
  NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
  ADDRESSEE: John H. C. Blasdale
  STREET: One Giralda Farms
  CITY: Madison
  STATE: New Jersey
  COUNTRY: USA
  ZIP: 07940-1000
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: Apple Macintosh
  OPERATING SYSTEM: Macintosh 6.0.5
  SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US93/07261
  FILING DATE: 19930805
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/927,531
  FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
  NAME: Blasdale, John H. C.
  REGISTRATION NUMBER: 31,895
  REFERENCE/DOCKET NUMBER: DX0288K
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 201-822-7398
  TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 10:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4766 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA to mRNA
  ORIGINAL SOURCE:
    ORGANISM: Plasmodium falciparum
    STRAIN: Malayan Camp
  IMMEDIATE SOURCE:
    CLONE: p2b1.p12-1
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 3..4766
  PCT-US93-07261-10
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Qy   363 ------IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThr 380
         |||                    ||||||||||::::|||
Db  2492 ATGCATATTACTAAAGAATTAAAAAATTGAAAATTCACACTGTTTTTTACAATAAAACACT 2551

Qy   381 GlyAlaGluAsp------LeuPheGluAsnLysIleGlyInGlyThrValAspPheIle 398
         ||| |||           ||| |||        |||         |||   |||
Db  2552 ATGCAACAGGAAAAGTATTCTTCAAGAGACTAATATC---CAACCAAATCTTGATATGATC 2608

Qy   399 AsnAsnGluIleArgAspProSerLysAlaLeu--------------------------- 409
         ||||||||||::|:||       :::
Db  2609 AAAAATGAAGTACTGACTCTTATGAGAACCATGCAAGAAAAAGCTGAACTAATGTACACAA 2668

Qy   410 ------IleArgLysValTyrThrGluAlaAspLeuPheGlu------------AsnLys 424
         :::||::||||       |||                       |||
Db  2669 GACTGTGTGAAGAAAATTTTAAACGAATCTCCTAAATTCTTCAATGTTCGTTATTGAGAAA 2728

Qy   425 IleGlyGlnGlyThrValAspPhe----------IleAsnLysGluIleArgAspProSerLys 442
         |||      |||                      |||      ||||||||||::|
Db  2729 ATCGAACATAATAAGCAGTAGAATTTCCAAAAAATTTTTATTAAAATATPAGCCGAGAAT------2782

Qy   443 AlaLeuIleArgLysValSerThrGluAlaAspAsnLeu 455
         ||| |||        |||         ::|
Db  2783 ------CTTTCTGATATTAGCGAAGAGAAAATAACACATG 2815
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US-09-807-459-2 (1-458) x PCT-US93-07261-10 (1-4766)

Alignment Scores:
  Pred. No.:                    0.000464    Length:       4766
  Score:                        119.50      Matches:      58
  Percent Similarity:           48.11%      Conservative: 31
  Best Local Similarity:        31.35%      Mismatches:   65
  Query Match:                  5.07%       Indels:       31
  DB:                           5           Gaps:         14
```

```
Qy   294 AsnLysGluIleArg---GluProSerLysAlaLeuLeuLysGluThrAspThr 312
         |||||||||::|||   ::|||         |||||||||::|::|||
Db  3135 AATAAAGAAATTACGAAATAAAGGATCTGAAGGATTAAAAGAAAATGCAGAACTAAAAAAT 3194

Qy   313 LysAspLeuPheGluAsnLysIleGlyInGlyGly------------ThrValAspPheAsn 329
         ||||||||||:::|||         |||               |||   |||
Db  3195 AAAGAATTA---CAAAATAAAGGATCTGAAGGATTAAAAGAAAATGCAGAATTAAAAAAT 3251

Qy   330 LysGlyIleArgAspPro----------SerLysAlaLeuLeuLysGluValSerAsnAspAlaLys 348
         ||||||||||::|          |||:||||||||||||::|||
Db  3252 AAAGAATTACAAAATAAAGGATCTGAAGGATTAAAAGAAAATGCAGAGCAAAAAAATAAA 3311

Qy   349 AspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArg 368
         ::|||||||||        |||         |||         |||   |||
Db  3312 GAATTA---CAAAATAAAGGATCTGAAGGATTAAAAGAA-----AATGCAGAATTAAAA 3362

Qy   369 AspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGlyAspLeuPheGlu-- 387
         :::|||||||||         |||         ||::|         |||:::|||
Db  3363 -----AATAAAGAAATTACGAAATAAAGGATCTGAAGGATTAAAAGAAAATGCAGAGCTA 3416

Qy   388 ------------------AsnLysIleGlyInGlyGly------------ThrValAspPheIle 398
         ||||||                              :::
Db  3417 AAAAAATTAAAGAATTACGAAATAAAGGATCTGATGGATTAAAAGAAAATGCAGAATTAAAA 3476

Qy   399 AsnAsnGluIleArgAspPro---SerLysAlaLeuLeuIleArgLysValSerThrGlyAlaGly 417
         ||| |||         ||:::|||         ||:||         |||||||||
Db  3477 AATGATTTAAAGAATAACGAATATT-----CAAAATAAAGAAATTACGAAATAATGCAGA 3533

Qy   418 AspLeuPheGluAsnLysIleGlyInGlyThrValAspPheIleIle 437
         |||         |||         |||         |||   |||
Db  3534 AATGATTTAAAGAATAACGATATT---CAAAATAAAGATTTACGTAAATAATAAAAAGACATG 3587

Qy   438 ArgAspProSerLysAlaLeuIleArgLysValSerThrGluAlaAspAsp----------- 453
         |||      ||:::|||         |||         |||
Db  3588 AAA------AATAAAGAACTATTAAACAAAAGATATATTTCTAATAAAGCACAGAAGAATAAA 3641

Qy   454 AsnLeuLeuGluLys 458
         ||||||    |||
Db  3642 GAACTATTAAATAAA 3656
```

```
RESULT 8
US-08-484-105-13
Sequence 13, Application US/08484105
Patent No. 5589341
GENERAL INFORMATION:
  APPLICANT: STILLMAN, Bruce
  APPLICANT: BELL, Stephen P
  APPLICANT: KOBAYASHI, Ryuji
  APPLICANT: RINE, Jasper
  APPLICANT: FOSS, Margit
  APPLICANT: McNALLY, Francis J
  APPLICANT: LAURENSON, Patricia
  APPLICANT: HERSKOWITZ, Ira
  APPLICANT: LI, Joachim J
  APPLICANT: GAVIN, Kimberly
  TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
  NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
  ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
  STREET: 4 Embarcadero Center, Suite 3400
  CITY: San Francisco
  STATE: California
  COUNTRY: USA
```

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;   ZIP:  94111-4187
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/484,105
;   FILING DATE:
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Osman Ph.D., Richard Aron
;   REGISTRATION NUMBER:  36,627
;   REFERENCE/DOCKET NUMBER:  A-59032/DJB/RAO
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 494-8700
;   TELEFAX:  (415) 494-8771
;   TELEX:  910 277299
;   INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  3278 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  double
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA

US-08-484-105-13

Alignment Scores:

Pred. No.:                              0.00283
Score:                                  111.00
Percent Similarity:                     35.50%
Best Local Similarity:                  19.33%
Query Match:                            4.71%

DB:

Score:                                  111
Matches:                                3278
Conservative:                           98
Mismatches:                             82
Indels:                                 199
Gaps:                                   128
                                        22
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US-09-807-459-2 (1-458) x US-08-484-105-13 (1-3278)

Qy      5 AspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSerAla 24
          :::|||||                      :::              |||
Db   1214 GAAGCTATATCAGATAATGACATCGGATTTATCTGAATATCACGAAAAGTAAAGAGAGTTT 1273

Qy     25 AlaAsnAlaTyrMetIleAsnSerAsp----------MetSerAspTyrLeuSerAlaSer 42
          ||||||||||                         ||||||        |||||| |||
Db   1274 GCAAACGCCATCCTCTTCGGACAGTGATGAAGAGTTGAAGAGTTACCAGTCTGCAGAGAG 1333

Qy     43 AspAsnPheAlaGlnArgIleCysSerGlnVal--------------------------- 53
          |||
Db   1334 CTTGCAATTGTAGAACCTGCCAAGAAAAAGGTGAGATCTATTAAACCAGATATACCCATT 1393

Qy     54 ---ProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSer---------Arg 69
          |||                                         :::   :::
Db   1394 TCACCAGTAAAAATCAGACACTCCATTGCAGCCATCAGCAGTGTTCATCTCATCTCCTAGAAAG 1453

Qy     70 CysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGlnAlaLysTyr 89
          |||
Db   1454 TTCTTTAAGAATAATAATAAGTCGCGCGCTAAAAAGGCATAATACTCCATTTCCAAACGGTAT 1513

Qy     90 GlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAlaPheIleLeuPheLysGlu 109
          |||                      ::|||||            :::
Db   1514 AAGAATCCGAAGATTCCTGACTTGAACGAT---------------ATTTTCCAAAGGCAT 1558

Qy    110 SerAspAlaAsnProAlaAsnSerThrGluLysArgPheThrTrpMetArgPheArgGly 129
          :::|||:::                ||||||||||||
Db   1559 AATAATGATTTGGATATAGCTGCCATTAGAGAGAGGAATTCAGAACACAGTTTCTCTAAAGGC 1618

Qy    130 LysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuLysAsnValThrArg 149
          |||                       |||          |||
Db   1619 AAAATGGAGACTATATTTTTTCTAAGGTCAAGAAGCAATTGAAGACTCAAGAATAGCAAAGAA 1678

Qy    150 Asp---AlaSerAlaThrAspIleGluAsnPhe----AlaSerArgTyrLeuTyrMetAla 167
          |||  :::|||                       :::|||
Db   1679 GAAATTGTCAAAGCTGCTGATTTCGACAATTATCTCCGGCACAATTATGAATTGCA 1738
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Qy      ʔ
Db   1739 AGTATAATACCTCTCCACTTTACAGTTGCAATT--- 1795
```

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Qy    168 ThrLeuTyrTyrLysThrTyrThrAsnValAspGluProGlyAlaSerPhePheAsnLys 187
          ::::::::|||                     :::           |||  |||
Db   1739 AGTATAATACCTCTCCACTTTACAGTTGCAATT---GAAGCAGGCACTAGCACCAGTATTTAC 1795

Qy    188 LeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysLysArgGlnIleIle 207
          :::::::|||            |||         :::::::
Db   1796 ATTGCCGGGACGCGCCAGGCGTT----------GGTAAAACTTTGACGGTTCGAGAGGTAGTT 1846

Qy    208 ArgSerAsnLeuProLeuAspIleGlyThr----------GluHisSerValSerArgLeu 224
          :::::::            ||:::|||                 |||
Db   1847 AAG---------------GATTTAATGACATCTGCAGACCAAAAAGAACTTCCAAGATTC 1891

Qy    225 GlnHisIle------------------------------------ThrSerSerTyrLys 232
          |||
Db   1892 CAATACATTGAAATCAATGGTTTAAAGATTGTCAAAGCAAGTGATAGTGTCTTT 1951

Qy    233 ----------------------------------AspTyrMetAspPhe 237
          |||                              :::
Db   1952 TGGCAAAATATCTGGAGAAAAGCTTACATCTGGAGCTGCCATGGAATCTCTGGAGTTT 2011

Qy    238 GlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnLeuArgLeu 257
          ::|||                              |||
Db   2012 TATTTTAACAAAGTGTTCCAGCTACGAAAAAAAGTCCTATCGTTGTGTTTATTGGATGAGCTT 2071

Qy    258 LeuAlaThrValAlaLGlyTyrValAspThrProTrp---TyrLysLysTyr----Tyr 274
          |||                           |||::::           :::
Db   2072 GATGCATTAGTTAGCAAGACCCAAGACTGTAATGTGATGTTACAACTTCTTTAACTGGGCTACCTAT 2131

Qy    275 MetLysLeuLysAsnPheMetVal----AsnArgValPheIleProThrLysLys 291
          |||::|||             |||
Db   2132 TCAAATGCGAAAACTTATTGTTGTAGCTGTGCGCAAACACCTTAGATCTCCCCGACGGCCAT 2191

Qy    292 PhePheAsnLys------------------------------------ 295
          :::|||||
Db   2192 CTTGGTAACAAGATTTCGTCCGAGAATTGGTTTTACTTAGAATTATGTTCACTGGTTACACG 2251

Qy    296 ------GluIleArg--------------------------------- 298
          |||::::|||
Db   2252 CATGAAGAGCTTAGAACAATCATCAAATTTGAGACTTAAATATATTGAACGAGAATCGTTTC 2311

Qy    299 -----GluProSerLysAlaLeuGlyLysValSerThrArgLysAspLeuPhe 316
          ::|||                           |||
Db   2312 TATGTCGACCCGGAGACAGGGAGGTTCGTACATGAATCTCCCGGATAGTAGTACTATA--- 2368

Qy    317 GluAsnLysIleGlyGlnGlyThrValAspPhePheAsnLysGlyIleIleArgAspProSer 336
          |||                              |||||
Db   2369 GAAACTGATGAGAGAGATGAAAAAGCGAAAAAGCAACTTCTCTAAC--------TAT 2410

Qy    337 LysValAlaLeuLysLysGlyValSerAsnAspAlaLysSerLeuPheGluAsnLysIleGly 356
          |||                              |||
Db   2411 AAACGACTAAAAACTTAGGATTAATCCTGATGCCATTGAGATTGCATCAAGAAAAAAATTGCT 2470

Qy    357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376
          :::|||                        |||:::
Db   2471 AGT-----GTCAGTGGTGATGTGCCGGAGAGCTTTAAAGTGGTTGTCAAAAGA 2515

Qy    377 LysValSerThrGlyAlaGluAspLeu----------PheGluAsnLysIle--- 390
          |||                      |||
Db   2516 GCGGTAGAATATGCGGGAAAAATGATTACTTAACTTGAGGCTTAACGGACTAGTCAAT 2575

Qy    391 -----GlyGlnGlyThrValAspPheIleAsnAsnGluIle 402
          |||                                  :::
Db   2576 TCCAAAAAAAGATACTTAGTGCCAATGGTACAGGAGAAATGAACAGTTAACAGTGTAGAAATT 2635

Qy    403 ArgAspProSerLysAlaLeu 409
          :::|||||||
Db   2636 AAGCATATTTACCAAGGCATTA 2656
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```
RESULT 9
US-08-484-106-13

; Sequence 13, Application US/08484106
; Patent No. 5614618
; GENERAL INFORMATION:
```

APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: MCNALLY, Francis J
APPLICANT: LAURENSON, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3278 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-08-484-106-13

US-09-807-459-2 (1-458) x US-08-484-106-13 (1-3278)

Alignment Scores:

Pred. No.:	
Score:	0.0283
Score:	111.00
Percent Similarity:	35.508
Best Local Similarity:	19.338
Query Match:	4.718
DB:	1

Length:	3278
Matches:	98
Conservative:	82
Mismatches:	199
Indels:	128
Gaps:	22

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Qy      5 AspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSerAla   24
          :::::::::||                                           |:::
Db   1214 GAAGCTATATCAGATAATGAATCGGATTTATTCTGAATACACGAAAGTAAAGAGAGTTT   1273

Qy     25 AlaAsnAlaTyrMetIleAsnSerAsp------------MetSerAspTyrLeuSerAlaValSer   42
          |||||||||||                         |||||| |||||
Db   1274 GCAAACGCATCCTCTTCGACAGTCAGTGATGAAGAGTTTGAGATTACCAGTCGCAGAGAAGAG   1333

Qy     43 AspAsnPheAlaGluArgIleCysSerGlnVal------------                      53
          |||                                      |:|||
Db   1334 CTTGCAATTGTAGAACCTGCCAAGAAAAAGGTGAGATGTCTATTAAACCAGATATACCCATT   1393

Qy     54 ---ProLysGlySerAsnCysSerAlaSerAlaTyrMetSer------------Arg       69
          |||           |||||                       |||         :::
Db   1394 TCACCAGTAAAATACACAGACTCCATTGCAGCCATCAGCACGTTCATTCCTTGAAAG       1453

Qy     70 CysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGluAlaLysTyr     89
          |||      :::                                      ::  :||
Db   1454 TTCTTTAAGAATAATATAGTGCGCGTCTAAAAAGGCATATACTCCATTTTCAAACGGTAT   1513

Qy     90 GlnProLeuThrLeuProAspProTyrGlnLeuGluLeuAlaAlaAlaPheIleLeuPheLysGlu  109
          |||                                                      |||
Db   1514 AAGAATCCGAAGATTCCTGACTTGAACGAT------------------------ATTTTCCAAAGGCAT  1558

Qy    110 SerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrpMetArgPheArgGly      129
          :::                   |||                           |:|  |||
Db   1559 AATAATGATTTTGGATATATAGCGTCCATTAGAGGAGGAGATTCAGAACAGTTTCTGCTAAGGC  1618

Qy    130 LysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGluLysAsnValThrArg    149
          |||                                      :::         |||
Db   1619 AAAATGGAGACTATATTTTTCTAAGGTCAGAAGAAGCAAATTGAACTCAAGGAATAGCAAAGAA  1678

Qy    150 Asp---AlaAspAlaThrAspIleGluAsnPhe---AlaSerArgTyrLeuPheTyrMetAla   167
          |||                               |||         :::
Db   1679 GAAATTGTCAAAAGCTGCTGATTTCGACAATTATCTCCGGCAACAGAAAAATGAATTTGCA   1738

Qy    168 ThrLeuTyrTyrLysThrTyrThrArgAsnValAspGluProGlyAlaSerPheAsnLys    187
          :::|||                                    |||
Db   1739 AGTATATACCCTCACTTTACAGTGCAATT---GAAGCAGGCACTACGACCACCAGTATTTAC   1795

Qy    188 LeuSerPheThrThrGlyIleLeuPheGlyTrpGlyIleLeuLysArgAlaLeuLysGlnIleIle  207
          :::|||                                    |||
Db   1796 ATTGCCGGCGACCCCAGGCGGTT---GGTAAAACTTTGACGGTTCGAGAGGTAGTT      1846

Qy    208 ArgSerAsnLeuProLeuAspIleGlyThr------GluHisSerValSerArgLeu      224
          |||                            |||
Db   1847 AAG------GATTTAATGACATCTGCAGACCCAAAAAGAAACTTCCAAGATTC         1891

Qy    225 GlnHisIle------------ThrSerSerTyrLys                             232
          |||                |||:::
Db   1892 CAATACATTGAAATCAATGGTTTAAAGACAGTCAAGTGATAGTTATGAAGTCTTT       1951

Qy    233 ------------AspTyrMetAspThr                                      237
          |||
Db   1952 TGGCAAAAAATATCTGGAGAAAAGCTTACACATCTGGAGCTGCCATGGAATCTCTGGAGTTT  2011

Qy    238 GlnIleIleProAlaLeuProLysPheSerLeuMetValValGlnArgLeu            257
          |||                                         :::
Db   2012 TATTTTAACAAAGTTCCAGCTACGAAAAAACGTCCTAATCGTTGTGTTATTGATGAGCTT   2071

Qy    258 LeuAlaThrValAlaIleGlyTyrValAspThrProTrp------TyrLysLysTrp------Tyr  274
          |||                             |||                  |||
Db   2072 GATGCATTAGTTAGCAAGAGCCAAGATGTAGATACAACTTCTTTAACTGGCTACCTTAT    2131

Qy    275 MetLysLeuLysAsnPheMetVal------AsnArgValPheIleProThrLysLys      291
          |||                    |||  :::
Db   2132 TCAAATGCCAAAACTTATTGTCTGTAGCTGTCGCGAAAACACCTTAGAATCTCCCGAACGGCCAT  2191

Qy    292 PhePheAsnLys------                                               295
          |||
Db   2192 CTTGGTAACAAGATTTGTCCAGAAATTGGTTTTACTAGAATTATATGTTCACTGGTTACACG   2251

Qy    296 ------GluIleArg                                                  298
          |||:::|||
Db   2252 CATGAAGAGCTTAGAACAACATCAATTGAGACTTAAATATATTGAACGAATCTAGTTTC    2311

Qy    299 -----GluProSerLysSerAlaLeuLysGluLysValSerThrAspThrLysAspLeuPhe   316
          |||                                      ::||
Db   2312 TATGTCGACCCGGAGCAGGAGAGTTGCTACACTGATCTCTCCGGATACTAGTACTATA---   2368

Qy    317 GluAsnLysIleGlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSer    336
          |||                                      |||
Db   2369 GAAACTGATGAAGAAGAGAAAAAGCGAAAAAGACTTCTCTAC------              2410

Qy    337 LysAlaLeuLysGluLysValSerAsnAspAlaLeuPheGluAsnLysIleGly         356
          |||:::                                    |||||||
Db   2411 AAACGACTAAAACTAGGATAATAATCCTGATGCCATCAGAATTGCAAGAGAAAAATTGCT   2470

Qy    357 GlnGlyThrValAspPheIleAsnAsnGlyIleIleArgAspProSerLysSerAlaLeuIleArg  376
          |||:::                                    |||:::
Db   2471 AGT---------------GTCAGTGGTGATGTGCGGAGAGCTTTAAAGGTGGTGTCAAAAGA   2515
```

```
Qy    377 LysValSerThrGlyAlaGluAspLeu----------------PheGluAsnLysIle--- 390
               |||           :||||||        :::|||
Db   2516 GCGGTAGAATATGCGAAAAATGATTACTTAAGAGAGGCTTAGATATGAGCGACTAGTCAAT 2575

Qy    391 -------------GlyGlnGlyThrValAspPheIleAsnAsnGluIle 402
                          :::       |||||||        :::
Db   2576 TCCAAAAAAGTATACTAGTGGCAATGGTTACAGGAAAATGAAGAATTACAGAGTGTAGAAATT 2635

Qy    403 ArgAspProSerLysAlaLeu 409
               :::||||||||||
Db   2636 AAGCATATTACCAAGGCATTA 2656
```

RESULT 10
US-08-694-869-2
Sequence 2, Application US/08694869
Patent No. 5994123
GENERAL INFORMATION:
APPLICANT: Olszewski, N.
APPLICANT: Tzafrir, I.
APPLICANT: Somers, D. A.
APPLICANT: Lockhart, B.
APPLICANT: Torbert, K.
TITLE OF INVENTION: SUGARCANE BACILLIFORM VIRUS
TITLE OF INVENTION: PROMOTER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,869
FILING DATE: 09-AUG-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.369US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
TELEFAX: 612-339-3061
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA

US-08-694-869-2

Alignment Scores:
Pred. No.:
Score: 0.0232
Score: 108.50
Percent Similarity: 34.95%
Percent Identity: 20.42%
Best Local Similarity: 4.60%
Query Match: 2

Length: 7568
Matches: 97
Mismatches: 154
Conservative: 69
Mismatches: 154
Indels: 155
Gaps: 24

US-09-807-459-2 (1-458) x US-08-694-869-2 (1-7568)

```
Qy     51 SerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSerArgCys 70
```

```
Db   1646 TCAGAGAATGCAGGTCAGTCAAGCACTTGCTTTTCT-----ACGGGTTACCTCAGACGACCC 1699
               |||                 :::  |||   |||::          |||:|||
Qy     71 AlaLysGlnAsp--------------------------CysLeuThrLeuGln-SerLeuGly 82
          :::|:|||                                  ||| |||||||  |||:|||
Db   1700 GAGAGAGAGAGAACCCTGGAGAGATGCTCATCGAGCCTGATGTGGAGCTNAACCAGGACGATGAA 1759

Qy     82 s------------------TyrProLeuGluAlaLysTyrGlnPro------------ 91
          :                  :::|||      ||| |||
Db   1760 GAAGAGAGCCCAGAGCTTTCCCAGCAGAAGTTCTGTATGCCCAGAAGTGTGATATTCA 1819

Qy     92 ----------------------------LeuThrLeuProAspProTyrGlnIle 100
                                        ||| :||||||     |||
Db   1820 TCACAAAGTCTTTCAAGGAGAGCTCTAGCCAGGATATCCTCCTGATTGATGACAATCAGCT 1879

Qy    100 uGluAlaLysAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluGly 120
          |||||||       :::|||           |||
Db   1880 TGATATGACCTTTATC------------------------------------------AAGGAGGA 1903

Qy    120 sArgPheTrpmetArgPheArgArgGlyLysAsnHisSerThrTyrPheHisAsp------ 137
            :::       |||     |||        :::
Db   1904 AACATTCGAGCAATTGGACCAGGCAGGACGTCCGG-----TATATTCATCCCGGAAATACT 1957

Qy    138 ------------------------------------------------------------ 138
Db   1958 AGCTGTTAGAATACAGCCCTCGACATGAGACTGGTCAGGAAAAACTGGGTTTTCATAGTTTT 2017

Qy    140 eAsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaAlaThrAspIleGlu--AsnPh 159
              |||           :::          |||
Db   2018 CCGTGACATCAGATAACCCACCAAGAGTACTTGGAGCTTATGGAAATTGATCTGAGCAA 2077

Qy    159 eAlaSerArgTyrrLeuTyrMetAlaThrLeuThrTyrrLysThrTyrThrAsnValAspGl 179
           :::|||:|||          |||           :::
Db   2078 AGGACCACCAAAATGGTTCTATGGTAGCATCAATAGCTTCAATGACAACGATAAAAGGAT 2129

Qy    179 yTrp---GlyIleLysArgAlaLeuLysGlnIleIleIleArgSerAsnLeuProLeuAspIl 196
              |||   |||                 :::
Db   2130 -----TTCTTTCATGGAATCCAGCTTACTGTTCACGTTGAAGGGTTATGAAGG 2176

Qy    196 uPheGlyAlaSerPheAlaLeuProAlaLeuArgPheSerLeuMetValValGl 215
           |||||       |||
Db   2177 TTGGCAAGGA-----------GAGGCCAACTTACACATTGAA 2207

Qy    215 eGlyThrGlyGluHisSerValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMe 235
             :::|||||||          :::     |||
Db   2208 -----AGGTTGATAAACTGCAAGATTGTCAAATACACCAATGTGTATTCAAGTAT-- 2258

Qy    235 tAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMetValValGl 255
              :::          |||  |||
Db   2259 -----AAGGTTGAAGGAGTGGCCGTCTTTTATCAAGACCAAAGGTATAAAAGCTATTGA 2311

Qy    255 nArgLeuLeuAlaThrValAlaLaGlyTyrValAspThrProTrpProTyrLysLysTrpTyrMe 275
            :::|||       ||| |||
Db   2312 AGCCACTAAAAAAGAGTGTGAAGGGCATCAGAGAGGAGGAGAATGGAAC-------- 2357

Qy    275 tLysLeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLy 295
              |||          :::|||
Db   2358 -----ATTCTCCATCAAAGCTA----- 2377

Qy    295 sGlyIleLeuArgGluProSerLysLysGluLysValSerThrArgThrLysAspPhe 315
           |||||||          |||
Db   2378 GGTAGTCATGCAACCTACC---AAGGTGCAGACTACA----- 2411

Qy    315 uPheGluAsnLysIleGlyGlnGlyThrValAspPheIleLeuAsnLysGluIleArgAspPr 335
           |||          |||  :::
Db   2412 ----GAAAATTATGATGGCACAACATCCTTCAGATTCACAAATTATGAAGGTGCCAGTTC 2467

Qy    335 oSerLysAlaLeuLeuLysGlyLysValSerAsnAspAla---LysAspLeuPheGluAsnLy 354
           |||||||          :::|||||||
Db   2468 TTCAAAAGCCAGTAGACACAAACTCAGATGATGAGGCCATATATACGGCCTCTTTGAAGAAGA 2527

Qy    354 sIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLe 374
           :::           |||  ::
```

```
Db   2528  AGAGGAAGAGGGATGACATCACTTCCTCAACCGA-----------------------AT 2563
Qy   374   uileArgLysValSerThrGly--------------AlaGluAspLeuPheGluAsnLysIl 390
Db   2564  CTTATCAAAGTACTCTACGGCAGCAAAAGGTAGTGGGAGAAGAAGAATTTTCCCAGAAGA 2623
Qy   390   eGlyGlnGlyThrValAspPheIleAsnAsn-----------------GluIleAr 403
Db   2624  AGACCAGATTATTTCTGATTTTCTTGGAAAAACTGAAGAAGAGCCTACCCTGTGAAATTGA 2683
Qy   403   gAspProSerLysAlaLeuIleArgLysValTyrThrGluAlaAspAspLeuPheGluAs 423
           |||||||      |||                                 :::||   |||
Db   2684  AGAAGAGTACCAGCCGCTAAGAGA                         CTTGAACAACTCATGAAAAC 2728
Qy   423   nLysIleGlyGlnGlyThrValAspPheIleAsnLysGluIleArgAspProSerLysAl 443
Db   2729  AAAAGTT------------GTTGTTCAAGAGATTGAAGAGCCATTCCCAGCC 2767
Qy   443   aLeuIleArgLysValSerThrGluAla-AspAsnLeuLeu 456
           :::|||||||||  |||||||||||||
Db   2768  AGTTGAAGCTAAGATGAGTACAGACACTGGATCATCTGCTA 2808
```

RESULT 11
US-09-349-546-2
; Sequence 2, Application US/09349546
; Patent No. 693569
; GENERAL INFORMATION:
;   APPLICANT: Olszewski, N.
;   APPLICANT: Tzafrir, I.
;   APPLICANT: Somers, D.A.
;   APPLICANT: Lockhart, B.
;   APPLICANT: Torbert, K.
;   TITLE OF INVENTION: Sugarcane bacilliform virus promoter
;   FILE REFERENCE: 600.369US2
;   CURRENT APPLICATION NUMBER: US/09/349,546
;   CURRENT FILING DATE: 1999-07-08
;   EARLIER APPLICATION NUMBER: US 08/694,869
;   EARLIER FILING DATE: 1996-08-09
;   EARLIER APPLICATION NUMBER: PCT/IB97/01338
;   EARLIER FILING DATE: 1997-08-13
;   NUMBER OF SEQ ID NOS: 10
;   SEQ ID NO 2
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO: 2
;   LENGTH: 7568
;   TYPE: DNA
;   ORGANISM: sugarcane bacilliform virus
US-09-349-546-2

```
Alignment Scores:
Pred. No.:
Score:                  108.50              Length:         7568
Percent Similarity:     34.95%              Matches:          97
Best Local Similarity:  20.42%              Conservative:     69
Query Match:            4.60%               Mismatches:      154
DB:                                         Indels:          155
                                            Gaps:             24
```

US-09-807-459-2 (1-458) x US-09-349-546-2 (1-7568)

```
Qy    51  SerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSerArgCys 70
Db  1646  TCACAGAATCGACGGTCAAGCACACTTGCTTTTCT----ACGGGTTACCTTCAGACGACCC 1699
Qy    71  AlaLysGlnAsp-----------------CysLeuThrLeuGln-SerLeuTy 82
Db  1700  GAGAGAAGAAGACCCTGGAGAATGCTCATGCAGCCTGAGTGGGAGCGTAACCAGGAGCA 1759
Qy    82  s----------------TyrProLeuGluAlaLysTyrGlnPro------- 91
Db  1760  GAAAGAGAGCCAGAGCTTTCCCACGAGAAGTTCTGTATGGCCGAGATGATGATATTCA 1819
Qy    92  ------------LeuThrLeuProAspProTyrGlnLe 100
Db  1820  TCACAAAGTCTTTCAAGGAGCTCTAGCCAGGNTATCCTCCTGATTGATGACAATCAGCT 1879
```

```
Qy   100  uGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLy 120
          |:::|                           |||                      |||::
Db  1880  TGATATGACCTTTATC-------------------------AAGGAGGA 1903
Qy   120  sArgPheTrpMetArgPheArgGlyLysAsnHisSerTyrProPheIleSerAsp----- 137
Db  1904  AACATTCCAGCAATTGGAGCAGGCAGAGACTCCGG-----TATATTCATTCCCGGAATACT 1957
Qy   137  -GlyThrValAspPheIleAsnAsn-----------------LeuValPh 140
Db  1958  AGCTGTTAGAATACAGCCTCTCGCATCCAGACTGGTCAGGAAAAACTGGTTTCATATTTT 2017
Qy   140  eAsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGlu--AsnPh 159
Db  2018  CCGTGACATCAGAGATAAACCCACCAAGAGTACTTGGAGCTAATATGGAATCTGAACAA 2077
Qy   159  eAlaSerArgGlyLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGl 179
Db  2078  AGGACCACAAAAGGTCTATTGTGATCAAGATTACACCAAATGTGTATTTCATGACACCAT 2129
Qy   179  uPheGlyAlaSerPhePheAsnLysLeuSerPheThrThr----------GlyLeuPheGl 196
          |||||||::::|                 |||                   |||
Db  2130  ----------TTCTTTCATGGAATCCAGCTTACTGTCAAGGTGAAGGGTTATGAAGG 2176
Qy   196  yITrp---GlyIleLysArgAlaLeuLysGlnIleIleIleThrSerSerArgCys 215
          |||       :::                            :::
Db  2177  TTGGCAAGGA-----------GAGGCCAACTTACACATTGAA-- 2207
Qy   215  eGlyThrGluHisSerValSerArgLeuGlnHisIleThrSerSerTyrArgLysAspTyrMe 235
Db  2208  ----------AGGTTGATAACTGCAAGATTTGTCAAATACAACCAAATGTGATTTTCAAGGTAT-- 2258
Qy   235  tAspThrGlnIleIleProAlaLeuProLysPheAlaLysArgPheSerSerLeuMetValValGl 255
Db  2259  ----------AAGGTTGAAGAGGTGGGCGTCTTTTATCAACAGCCAAAAGGTATAAAAGCTATTGA 2311
Qy   255  nArgLeuLeuAlaThrValAlaGlyThrValAspPheThrProTyrLysLysTrpTyrMe 275
Db  2312  AGCCACTAAAAAGAGTGTGAAGGGCATCAGAGGAGGAGGAAC---------- 2357
Qy   275  tLysLeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLy 295
Db  2358  ----------ATTCTCCATCAAAGCTA----------GA 2377
Qy   295  sGlyIleGluArgGluProSerLysAlaLeuLysGluLysGluLysSerValSerThrArgAspThrLysAsple 315
          :::|||||   |||                            :::||||||
Db  2378  GGTAGTCATGCAACCTACC----------AAGGTGCAGAACTACA---------- 2411
Qy   315  uPheGluAsnLysIleGlyGlnGlyThrValAspPheAsnLysGluIleArgAspPr 335
Db  2412  ----------GAAAATTATGATGGCACAACATCCTTCAGATTCACAAATTATGAAGGTGCCAGTTC 2467
Qy   335  oSerLysAlaLeuLysGlyLysGluLysSerValSerAsnAspAla--LysAspLeuPheGluAsnLy 354
Db  2468  TTCAAAGCCAGTAGAGCACAACTCAGATGATGAGGCATATATGGCCGCTCTTTGAAGAGA 2527
Qy   354  sIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLe 374
          :::                         |||||||||||::::
Db  2528  AGAGGAAGAGGGATGACATCACTTCCTCAACCGA----------AT 2563
Qy   374  uIleArgLysValSerThrGly----------AlaGluAspLeuPheGluAsnLysIl 390
Db  2564  CTTATCAAAGTACTCTACGGCAGCAAAAGGTAGTGGGAGAAGAAGAATTTTCCCAGAAGA 2623
Qy   390  eGlyGlnGlyThrValAspPheIleAsnAsn-----------------GluIleAr 403
Db  2624  AGACCAGATTATTTCTGATTTTCTTGGAAAAACTGAAGAAGAGCCTACCCTGTGAAATTGA 2683
Qy   403  gAspProSerLysAlaLeuIleArgLysValTyrThrGluAlaAspAspLeuPheGluAs 423
          |||||||      |||                                 :::||
Db  2684  AGAAGAGTACCAGCCGCTAAGAGA----------CTTGAACAACTCATGAAAAC 2728
```

```
Qy   423 nLysIleGlyGlnGlyThrValAspPheIleAsnLysGluIleArgAspProSerLysAl 443
             |||:||
Db  2729 AAAAGTT----------------------GTTGTTCAAGAGATTGAAGAGCCATCCCAGCC 2767

Qy   443 aLeuIleArgGlyValSerThrGluAla-AspAsnLeuLeu 456
             |||::|||||||                ||||
Db  2768 AGTTGAAGCTAAGATGAGTACAAGCACTGGATCATCTGCTA 2808
```

RESULT 12
US-08-453-8
Sequence 8, Application US/08453848
Patent No. 5583368
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Volovitz, Franklin
; APPLICANT: Wilkinson, Bethanie Eident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanway
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1766 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
; FEATURE:
; NAME/KEY: polyhedrin mRNA leader (partial)
; LOCATION: 1 to 18
; FEATURE:
; NAME/KEY: coding region for AcNPV 61K protein signal
; LOCATION: 19 to 72
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 19 to 72
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 76 to 81
; FEATURE:
; NAME/KEY: KpnI restriction site

; LOCATION: 82 to 87
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 88 to 93
; FEATURE:
; NAME/KEY: coding region for mature rHA
; LOCATION: 73 to 1734
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 1744 to 1749
; FEATURE:
; NAME/KEY: BglII restriction site
; LOCATION: 1750 to 1755
; FEATURE:
; NAME/KEY: universal translation termination signal
; LOCATION: 1756 to 1766
US-08-453-848-8

Alignment Scores:
Pred. No.:   0.0049   Length: 1766
Score: 105.50   Matches: 60
Percent Similarity: 36.06%   Conservative: 37
Best Local Similarity: 22.30%   Mismatches: 87
Query Match: 4.47%   Indels: 85
DB: 2   Gaps: 14

US-09-807-459-2 (1-458) x US-08-453-848-8 (1-1766)

Qy   195 PheGlyTrpGlyIleLysArgAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAsp 214
             ||||||| :::|||
Db   874 TTTGGGTCAGGA--------------------ATCATCACCTCAAACGCATCAAATGGAT 912

Qy   215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSerSer------TyrLys 232
             ||| |||||| :::
Db   913 GAATGTGACCGAAGTGTCAAACACCCCAGGAGGACTATAAACAGTAGTCTTCCTTTCCAG 972

Qy   233 AspTyrMetAspThrGlnIleProAlaLeuPheAlaLysArgPheSerLeuMet 252
                          ||| |||
Db   973 AATGTACACCCAGTCACAATAGGAGAGTCCAAAGTATGTCAGGAGTACAAATTAAGG 1032

Qy   253 ValVal--------------------GlnArgLeuLeuAlaThrVal 261
             :::||| |||
Db 1033 ATGGTTACAGGACTAAGGACAACATCCCATCCAATCCAGAGGTTTGTTTGGAGCCATT 1092

Qy   262 AlaGlyTyrValAspThrProTrp--------TyrLysLysTrpTyr-------- 274
             ||||:::::||| |||
Db 1093 GCCGGTTTCATTGAAGGGGGGTGGACTGGAATGATAGATGGTGTATGCATCATCAT 1152

Qy   275 --------------------MetLysLeuLysAsn 279
                                 |||
Db 1153 CAGAATGAACAAGGATCTGGCTATGCTGCGGACCAAAAAAAGCACACAAAAATGCCATTAAC 1212

Qy   280 PheMetValAsnArgVal------------------PheIleProThr 289
             |||:||| |||
Db 1213 GGGATTACAAACCAGGTGAAATTCTGTAATCGAGAAAAATGAACACTCAATTCACAGCTG 1272

Qy   290 LysLysPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysLysGluLysValSer 309
             ||| :::|||||||||||
Db 1273 GGCAAAGAATTCAACAAA--TTAGAAGAAGGAATGGAAAACTTAAATAAAAAGTTGAT 1329

Qy   310 ThrAspThrLysAsp--------------------LeuPheGluAsnLys 319
             |||||| ||||||
Db 1330 GATGGATTTCTGGACATTTGGACATATAATGCAGAAATGTTTGGTTTCTACTGGAAAAT-- 1386

Qy   320 IleGlyThrGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeu 339
             |||:::   :::
Db 1387 --GGAAGG---ACTTTGGATTTCATGACTCAAATGTTGAAGAATTCGTATGAGAAAGTA 1440

Qy   340 LysGluLysValSerAsnAsnAspAlaLysPheLeuPheGluAsnLysIleGlyGlyThr 359
             |||:::||||||||||:||||||||||||||:::
Db 1441 AAAAAGCCAATTGAAGAATAAATGCCAAAGAA----------ATAGGGAACGGGTGT 1485

Qy   360 ValAspPhe------------------IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376
```

Db 1486 TTTGAATTCTATCACAACAGTGTAACAACTGAA------------------------TGCATGGAA 1524
              ::::||||                                                    ::
Qy  377 LysValSerThrGlyAlaGlyLeuAspLeu-----------------PheGluAsnLysIleGlyGln 392
              |||   ||                        |||||:||||||:::
Db 1525 AGTGTGGAAAAAATGGAACTTATGACTATACCAAAATATTCCGAAGAATCAAAAGTTAAACAGG 1584
Qy  393 GlyThrValAspPheIleAsnAsnGlu 401
              ||| ||| :::
Db 1585 GGAAAAAATTGATCGAGTGAAATTGGAA 1611

RESULT 13
Sequence 8, Application US/09169027
Patent No. 6245532
GENERAL INFORMATION:
APPLICANT: Smith, Gale Eugene
APPLICANT: Volvovitz, Franklin
APPLICANT: Wilkinson, Bethanie Eldent
APPLICANT: Voznessensky, Andrei I.
APPLICANT: Hackett, Craig Stanway
TITLE OF INVENTION: A METHOD FOR PRODUCING MULTIVALENT INFLUENZA
TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,027
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/453,848
FILING DATE: 30-MAY-1995
APPLICATION NUMBER: 08/120,607
FILING DATE: 13-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MGS101CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1766 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Influenza virus
INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
FEATURE:
NAME/KEY: polyhedrin mRNA leader (partial)
LOCATION: 1 to 18
FEATURE:
NAME/KEY: coding region for AcNPV 61k protein signal
NAME/KEY: peptide
LOCATION: 19 to 72
FEATURE:

FEATURE:
NAME/KEY: Smal restriction site
LOCATION: 76 to 81
FEATURE:
NAME/KEY: Kpnl restriction site
LOCATION: 82 to 87
FEATURE:
NAME/KEY: Smal restriction site
LOCATION: 88 to 93
FEATURE:
NAME/KEY: coding region for mature rHA
LOCATION: 73 to 1734
FEATURE:
NAME/KEY: Kpnl restriction site
LOCATION: 1744 to 1749
FEATURE:
NAME/KEY: Bglll restriction site
LOCATION: 1750 to 1755
FEATURE:
NAME/KEY: universal translation termination signal
LOCATION: 1756 to 1766
US-09-169-027-8

US-09-807-459-2 (1-458) x US-09-169-027-8 (1-1766)

Alignment Scores:
Pred. No.:              0.0049              Length:        1766
Score:                  105.50              Matches:         60
Percent Similarity:     36.06%              Conservative:    37
Best Local Similarity:  22.30%              Mismatches:      87
Query Match:             4.47%              Indels:          85
DB:                          4              Gaps:            14

Qy  195 PheGlyTrpGlyTyrLeuTyrAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAsp 214
              |||||||                                    :::|||
Db  874 TTTGGGTCAGGA---------------------ATCATCACCTCAAACGCAATCAATTGGAT 912

Qy  215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleSerThrSer-----TyrLys 232
              ||| |||||||                               |||:||      :::
Db  913 GAATGTGACGGGAAGTGTCAAACACCCCAGGGAGGCTATAAACAGTAGTCTTCCTTTCCAG 972

Qy  233 AspTyrMetAspThrGlnIleProAlaLeuProLysProGlyPheSerLeuMet 252
              :::                                          |||||||
Db  973 AATGTACACCCAGTCACAATAGGAGAGTGTTCCAAAGTAATGTGCAGGAGTACAAAAATTAAGG 1032

Qy  253 ValVal------------------GlnArgLeuLeuAlaThrVal 261
              :::                      |||
Db 1033 ATGGTTACAGGACTAAGGAACATCCCATTCCAATTCAAATCCAGAGGGTTTGTTTTGGGACCATT 1092

Qy  262 AlaGlyThrTyrValAspPheThrProTrp-----------TyrLysLysTrpTyr----- 274
              ||||||||:::::::::                     |||               |||
Db 1093 GCCGGGTTTCATTGAAGGGGGGTGGACTGGAATGATAGATGGGTATGGTTATCATCAT 1152

Qy  275 -------------------MetLysLeuLysAsn 279
                                 |||
Db 1153 CAGAATGAACAAGGAGATCTGGCTATGCTGCGGACCAAAAAAGCCACACAAAAGCCATTAAC 1212

Qy  280 PheMetValAsnArgVal-------------------PheIleProThr 289
              :::   ||||:|||                         |||
Db 1213 GGGATTACAAACAAGGTGAATTCTGTAATCGAGAAATGAACACTCAATTCACACGTGTG 1272

Qy  290 LysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysLysValSer 309
              |||||||:::|||||||||                 :::|||||
Db 1273 GGCAAAGAATTCAAACAA-------TTAGAAGAAGGATGCAAAACTTAAATAAAAAGTTGAT 1329

Qy  310 ThrAspThrLysAsp-----------------LeuPheGluAsnLys 319
              |||                               |||:|||||
Db 1330 GATGGAATTCTGACAATTGGACATATAATCGAGAATTGTTGGTTCTACTGGAAAAT--- 1386

Qy  320 IleGlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeu 339
              |||:||||||||||||:::                    :::|||||:||||||||
Db 1387 ---GGAAGG---ACTTTGGATTTTCATGACTCAAAATGTGAAGAAATCTGTATGGAGAAAGTA 1440

Qy  340 LysGluLysValSerAsnAsnAspAlaLysSerAspLeuPheGluAsnLysIleGlyGlnGlyThr 359

```
Db   1441 AAAAGCCAATTGAAGAATAATGCCAAAGA----------------ATAGGGAACGGGTGT 1485
               ||||  ::::  |::::|||||||::::                   ||||||
Qy    360 Valaspphe--------IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376

Db   1486 TTTGAATTCTATCACAAGTGTAACAATGAA-----------------TGCATGGAA 1524
               :::|||   ||||||||||                              :::
Qy    377 LysValSerThrGlyValAlaGluAspLeu-----PheGluAsnLysIleGlyGln 392
               |||           |||          ||::::|||:::

Db   1525 AGTGTGAAAAATGGAACTTATGACTTATCCAAAATAATTCCGAAGAATCAAAGTTAAACAGG 1584

Qy    393 GlyThrValAspPheIleAsnAsnGlu 401

Db   1585 GGAAAAATGCATTGGAGTGAAATTGGAA 1611
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RESULT 14

US-09-091-117-3

Sequence 3, Application US/09091117

Patent No. 6171589

GENERAL INFORMATION:
  APPLICANT: The University of Melbourne
  TITLE OF INVENTION: Mycoplasma Recombinant Polypeptides and
  TITLE OF INVENTION: Vaccines
  NUMBER OF SEQUENCES: 5
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: GREENLEE, WINNER and SULLIVAN P.C.
    STREET: 5370 Manhattan Circle, Suite 201
    CITY: Boulder
    STATE: Colorado
    COUNTRY: United States of America
    ZIP: 80303
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/091,117
    FILING DATE: 12 JUNE 1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/AU96/00803
    FILING DATE: 13-DEC-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: AU PN7127
    FILING DATE: 13-DEC-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: WINNER, Ellen P.
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: +1 303 499 8080
      TELEFAX: +1 303 499 8089
  INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 4071 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    ORIGINAL SOURCE:
      ORGANISM: Mycoplasma pneumoniae
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 250..654
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 762..3851
      OTHER INFORMATION: /codon= (seq: "tga" 3648..3651, aa: Trp)
      OTHER INFORMATION: /codon=(seq: "tga" 3663..3665, aa:Trp)

US-09-091-117-3

Alignment Scores:
  Pred. No.:   0.026   Length: 4071
  Score: 104.50   Matches: 93
  Percent Similarity: 36.67%   Conservative: 68

Best Local Similarity: 21.18%   Mismatches: 173
Query Match: 4.43%   Indels: 105
DB: 4   Gaps: 21

US-09-807-459-2 (1-458) x US-09-091-117-3 (1-4071)

```
Qy    78 LeuGlnSerIleuLysTyrProLeuGluAlaLysTyrGlnPro------------Leu 92
             |||  |:::|||  :::|||  ||||||||:::                     |||
Db  1083 GCCAAGGCGCTTCCCAGCCTACCGCTGATTTACAGGAATGGGTTGACCAACAGCTGTTT 1142

Qy   102 AlaAlaPheIleLeuPheLysGlu-----------------------------SerAsp 111
             |||  :::|||  |:::                                     |||
Db  1023 TTAGCGGAAGAACGCGCCTTAAGGATAAACTCCAAGGTGGAGTTTGATAAATTCCTAAGTGAT 1082

Qy    93 ThrLeuProAsp--------------------------ProTyrGlnLeuGlu 101
             |||::::  :::                            ||| ||||||
Db   963 ACCGTGGAAAAACGGACTGATAAATTAGTCAACTATAAGTCTCACCACAACAACTCTTT 1022

Qy   130 LysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGluLysAsnValThrArg 149
             |||  |||:::                  :::           |||    |||
Db  1143 AATCCAAACCAAAGTTTCTTTGATTTA-----AGTGCGCGCCAGGTGAAAACTTTACCCTT 1196

Qy   150 AspAlaAspAlaThrAspIleGluAsnPheAlaSerArgThrLeuThrTyrMetAlaThrLeu 169
             |||  ::::|||                |||      |||
Db  1197 TCATCTGACAAAAAGGGCTAGTTTAGACTTTATCTTCCGC----------------------- 1235

Qy   170 TyrTyrLysThrThrTyrThrAsnValAspGluPheGlyAlaSerPhePheAsnLysLeuSer 189
             ||| ||||||                                          |||
Db  1236 ----------------TTTACTTAAC------------------------------------ 1244

Qy   190 PheThrThrGlyLeuPheGlyTrpGlyTyrIleLysArgAlaLeuLysGlnIleIleArgSer 209
             |||||||                   ::::|||          |||          :::
Db  1245 TTCACCGAAATCCGTTCAGTTGTTAAAAACTACCAGAAGGTGTATCGGTTGTAGCTGTTGACTCC 1304

Qy   210 AsnLeuProLeuAspIleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSer 229
             |||             ::::|||
Db  1305 AAACAAAAGCTTTGATTACTATGTCAAATGCTAGTGCCCAAAAATTATTAGTTGTACCGCTG 1364

Qy   230 SerTyrLysAsp------------------TyrMetAspThrGlnIleProAlaLeuPro 243
             |||             |||                                 |||
Db  1365 TCTTTACCCAGATTACACTTTTGGGTTTAAACTATATGTTTGACCACATTACTTTAAACGGT 1424

Qy   244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaAlaGly 263
             |||          :::|||                |||
Db  1425 AAGGTTGTCAATAAATTTAGTTTTAATCCGTTCAAAAACGAAATTAAACCTCGCC------ 1478

Qy   264 TyrValAspThrProThrProTyrLysTrpTyrMetLysLysAsnPheMetValAsn 283
             |||                ::::|||              |||
Db  1479 ------------TTTAGCAACGTTCATCAGTCGTTTGAAGCACAA 1520

Qy   284 ArgValPheIleProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAla 303
             |||          |||                   :::
Db  1521 AAGAATTTAGTAGGTAAGGGTAAATACCTCACCACCCACGTGAAG------GCTGAAGAC 1574

Qy   304 LeuLysGluLysValSerThrAsnThrLysAspLeuProPheGlu-------------- 317
             |||:::  |||                        |||
Db  1575 GTAAAGAAGGAGACGTTAATGCCAACATTAAAAACCAATTTGACATTGCCAAAATTATCGCT 1634

Qy   318 AsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnLysGlu-------------- 337
             :::||||||                       :::|||
Db  1635 GAGCTAATGGGTAAAGCCCTTAAAGAAGAATTTGGCAATCAACAAGAAGGTCAACCATTATCC 1694

Qy   338 AlaLeuLys-----------GluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIle 355
             |||:::                |||        |||        |||
Db  1695 TTCCTAAAGGTAATGGATAAAGGTAAAGCAGACGATTTTGAAAAACTGTTT---AACTTAGTC 1751

Qy   356 GlyLeuGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIle 375
             |||          |||                   :::|||        |||
Db  1752 CGTCCGTGGATTGGGGTAAAATTTGTTTGTAGGGGCCTTAATCCAAAGTAGTGACTTCAAGCA 1805
```

RESULT 15
US-08-688-988-7
Sequence 7, Application US/08688988B
Patent No. 6096545
GENERAL INFORMATION:
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PP196-03
CURRENT APPLICATION NUMBER: US/08/688,988B
CURRENT FILING DATE: 1996-07-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1407
TYPE: DNA
ORGANISM: Brassica Nigra
DB: US-08-688-988-7

Alignment Scores:
Pred. No.:

Score:	0.0595
Percent Similarity:	103.50
Percent Identity:	33.44%
Best Local Similarity:	20.20%
Query Match:	4.39%
	3

Length:	1407
Matches:	61
Conservative:	40
Mismatches:	88
Indels:	113
Gaps:	14

US-09-807-459-2 (1-458) x US-08-688-988-7 (1-1407)

```
Qy  376 ArgLysValSerThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrVal 395
            :::|||||||||||||:::|||||:::||||||
Db 1806 GAAAACAAGAUAACTGTCTACAAGAGTTAATCTTTGACAACAAA------AAGACCATC 1856

Qy  396 AspPheIleAsnAsnGluIleArgAspPro------------SerLysAlaLeuIleArg 411
            |||:::|||:::|||||                  |||:::|||
Db 1857 TTAAACCTACTTAAAGAGACTTTCCATTCCGAATTAAACTCTTCTTTAGGTTTAGTGGAC 1916

Qy  412 ------------LysValTyrThrGluAlaAspLeuPheGluAsnLysIleGlyGlnGly 428
                         |||:::|||||||||||||:::|||||
Db 1917 GTCTTGTTTGATGTCATTACTACTGACTCTGATGGTCTCTATGAAGAAGGTTG----CAATCT 1970

Qy  429 ThrValAspPheIleAsnAsnGluIleArgAspProSerLysAla----------- 443
            |||||||||:::|||                        |||
Db 1971 TTCAAAGACTTAATCGTTCCAGCAGTTAAAACGAATGAAAAAACCGCGGGCTTTAAGTCCA 2030

Qy  444 LeuIleArgLysValSerThrGluAlaAsp----------AsnLeuLeuGluLys 458
            |||:::|||                         :::|||
Db 2031 TTAATTGAAGAGTTTATTAACCCAAAAGGATACCTATGTGTTTGACTTAATTCAAAAA 2087
```

US-09-807-459-2 (1-458) x US-08-688-988-7 (1-1407)

```
Qy  181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyIleLeuLys 200
            |||||||||||||||||                  |||:::|||
Db  603 GGTGCATCCATTGACCGTGCCACTTGACTTT------------ATTTTGGGATGGCATCGGAC 653

Qy  201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
            |||:::||||||:::|||
Db  654 ACAACTATGTATGGAGATTATCCGCAGATCATGAAAGAT 692

Qy  221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyr------MetAsp 236
            |||   |||:::|||                         |||
Db  693 ATTGTTGGACATAGAATTGCTAAATTTACCGAA----------GCCACAGAAAGAT 737

Qy  237 ThrGlnIlePheAlaLeuProLysPheAlaLysAspPheSerLeuMetValValGlnArg 256
            |||||||||||||||||:::|||
Db  738 AAACTGAAAAACTCAGCCGATTTCGTCGGGCTCAACTATTAT-----------CCACAGAAAGCA 779

Qy  257 LeuLeuAlaThrValAlaGlyIleTyrValAspThrProTrpTyrLysTyrMetLys 276
            :::|||||||:::|||
Db  780 ------------------------------------------ACTTCGATGTTTCAAACCAT 800

Qy  277 LeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLysGlu 296
            |||:::|||
Db      779
```

RESULT 16
US-08-799-138-3
Sequence 3, Application US/0879913B
Patent No. 5994053
GENERAL INFORMATION:
APPLICANT: Verma, Desh Pal
TITLE OF INVENTION: PHRAGMOPLASTIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALFEE, HALTER & GRISWOLD
STREET: 800 SUPERIOR AVENUE
CITY: CLEVELAND
STATE: OHIO
COUNTRY: USA
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/799,138
APPLICATION DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLRICK, MARY E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 3:

```
Qy  297 IleArgGluProSerLysAla---------------LeuLysGluLysValSerThrAsp 311
            |||:::|||                         :::|||:::|||
Db  801 CTGGAGAAGCCAGCAATCCTGCTAAAACCAAGATGGATGCAAGAGTTCTTATTAACTGGAA 860

Qy  312 ThrLysAspLeuPheGluAsnLysIleGlyGln------------GlyThrValAspPhe 327
            |||:::|||||||||:::|||                         |||
Db  861 ACTAAGAAATCCGTACAATTACAGCATTGGTAGCAGCCTATCACCGGTGCCTGTTCCGGTT 920

Qy  328 PheAsnLysGluIleArgAspProSerLysAlaLeuIleArgLysValSerValAspAla 347
            ||| :::|||:::||||||
Db  921 TTTGCGAGAGGCTTTAGAAGTCTTTGAAGTACATCAAAGGATAAGTAATGGCCAACCCAGAA 980

Qy  348 LysAspLeuPheGluAsnLysIleGlyGln------------------ 357
            |||:::||||||||||||
Db  981 ATTATGATCATTGGAAAAACGGATATGGGGGCTGCAGATTCAATTGAAGTT 1040

Qy  358 GlyThrValAsp--------------PheIleAsnAsnGluIleArgAspProSerLys 372
            ||||||                         |||:::|||
Db 1041 GGTACAGCTGATCACAACAGGAAAATATTATCTTCAGAGGCATCTTTTGAGCATGAATGAA 1100

Qy  373 AlaLeu--IleArgGluValSer---ThrGlyAla------- 382
            |||:::|||                         :::|||
Db 1101 GCTATTTGCATCGACAAAGGTGAATGTTACCGGATACTTTGTATGGTGTCCTTGTTGGATAAC 1160

Qy  383 -----------GluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsn 399
                      |||:::||||||:::|||||||||:::||||||
Db 1161 TTTGAGTGGGCAAGATGGTTACAAGAACAGAACAGTTCGGACTTCTACTACATTGATTTCAAGAAT 1220

Qy  400 AsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyrThrGluAlaAspAsp 419
            |||:::|||
Db 1221 AACCTCACACGA------------------ 1232

Qy  420 LeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAsp 439
            :::||||||||||||:::||||||
Db 1233 ---TACGAGAAAGAGTCAGCCAGGTACTACACAAAGACTTCCTTAAGTCAAGTGTTCGT--- 1286

Qy  440 ProSer 441
            |||||||
Db 1287 CCATCC 1292
```

```
SEQUENCE CHARACTERISTICS:
  LENGTH: 2134 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
  NAME/KEY: CDS
  LOCATION: 127..1956
US-08-799-138-3

Alignment Scores:
Pred. No.:
Score:                          0.021
Score:                        101.50
Percent Similarity:            34.70%
Percent Identity:              17.48%
Best Local Similarity:          4.30%
Query Match:                        2
DB:

Length:         2134
Matches:          68
Conservative:     67
Mismatches:      127
Indels:          127
Gaps:             17
```

```
US-09-807-459-2 (1-458) x US-08-799-138-3 (1-2134)

Qy   139 ValPheAsnLeuLeuGluLysAsnValThrArgAspAlaThrAspIleGluAsn 158
              |||   |||
Db   955 AGAATGGGTTCCGACGATCTGGCGAAGATG 984

Qy   159 PheAlaSerArgTyrLeuThrTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAsp 178
         :::     |||        :::|||
Db   844 GTTGTGAATAGATCACAACAAGACATAAACAAGAATGTTGACATGATTGCTGCTAGGCGT 903

Qy   179 GluPheGlyTyrAlaSerPhePheAsnLysLeuSerPhethrThrThrGlyLeuPheGlyTyrProGly 198
         |||                              |||
Db   904 AGAGAAACGTGAGTAC---TTCAATAGTACCCCTGAATATAAACACCTTGCGAAC 954

Qy   199 IleLeuLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlu 218
         :::    ||||    ::|||    ::|||
Db   985 CTCTCAAAGCATTGGAGACAGTAATCAAGTCCAAAATTCCT 1035

Qy   219 HisSerValSerArg------- 223
         :::::::
Db  1036 TCTCTAATTACAAAACAAATTGCTGAACTTGAAGCTGAACTAACTCGTTTAGGAAAGCCT 1095

Qy   224 -----LeuGlnHisIleThrSerSer----- 230
         ||| |||
Db  1096 GTACGAGCTGATGCTGGGGAAAGTTGTATGCCAATCATGGAAATATGCCGCTCATTTGAT 1155

Qy   231 -----TyrLysAspTyrMet--- 235
         :::||||:::::
Db  1156 CAAATATTTAAAGACCATTCTTGATCGGCGTCGCGGCCTGGAGGTGATAAAATTTATAATGTC 1215

Qy   236 ---AspThrGlnIleProAlaLeuProLys------ 251
         :::|||||:::||||
Db  1216 TTTGACAAATCAGCTCCCCGCTGCTTTAAAAAGGTTGCAGTTTGATAAGCAGCTTTCAAATG 1275

Qy   252 MetValValGlnArgLeuLeuAlaThrhrValAlaGlyTyr------ValAspThrPro 268
             |||||                                      |||
Db  1276 GAAAATATAAGGAAACTTATTACTGAAGCTGCAGCCTCATCCTTATAGCTCCA 1335

Qy   269 TrpTyrLysLysTrpTyrMetLysLysLeu--LysAsnPheMetValAsnArgValPheIle 287
         :::||| ::||| ::||:
Db  1336 ----GAACAAGGATATCGTCGTTCAATTCTTCTAATAACT 1377

Qy   288 ProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLys 307
            |||||||   |||||||
Db  1378 ----ATTAGGGGCCCTGCTGAGGCAGCTGTTGATGCG 1410

Qy   308 ValSerThrAspThrLysAspLeuAsnLysSerIleGlyIleGlyThrGlyThrValAspPhe 327
         |||            |||||||||
Db  1411 GTTCACTCGCTGTTAAAGGACTTGGTTCAC 1440

Qy   328 PheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysGlyValSerAsnAspAla 347
         |||||||:: |||         |||
Db  1441 ----AAAGCTATCAGTGAGACTTTGGACTTGAAGCAG 1473
```

```
Qy   348 LysAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsnAsnGluIle 367
         :::
Db  1474 TATCCTGGTCTCCGGGTTGCAGGTTGGGCGTGGGCCTGCTCGTTGGTTGATTCACTA---GAAAGAATC 1530

Qy   368 ArgAspProSerLysAlaLeuIleArgLysLysValSerThrGlyAlaGluAspLeuPheGlu 387
         |||||||
Db  1531 ACGGATGAAAGCAAA------------------AGAGCAACACTCCAGCTAGTTGAT 1569

Qy   388 AsnLysIleGlyIleGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLys 407
         ||| ||| |||
Db  1570 ATGGAGTGTGGCTATCGACGTGTTGATTTCTTTCGGGAAGCTTCCTCAAGAATGTTGATAAG 1629

Qy   408 Ala-------------LeuIleArgLysValTyrThrGluAlaAspAspProLeuPheGluAsnLysIle 425
                         :::|||    ::|||
Db  1630 GGTGGCAATCCCACACATTCAATTTTGATAGATAATAATGATTCATATCTTAAGGCGAATT 1689

Qy   426 GlyGlnGlyThrValAspPheIleAsnLys------- 435
         ||||||  |||
Db  1690 GGAACCACAAATTTTGTCATATGTCAATATAGGTCTTGTGCTTCTGCTCTACACTGCGGAAATTCAATTCC 1749

Qy   450 ThrGluAlaAspAspAsnLeuLeuGluLys 458
         ||||||   |||
Db  1810 ACCGAGCTAGGCAAAATGGAGACCAAG 1836

Qy   436 -----------------GluIleArgAspProSerLysAlaLeuLeuIleArgLysValSer 449
                           :::|||    ::|||
Db  1750 AAGTCCATCGTCTTATTGTCAAGTCGCGGGGAGGCAAAACGAAGTCTACTTGATCACTTTTTT 1809
```

```
RESULT 17
US-09-392-362-3
Sequence 3, Application US/09392362
Patent No. 6248868
GENERAL INFORMATION:
  APPLICANT: Verma, Desh Pal
  TITLE OF INVENTION: PHRAGMOPLASTIN
  NUMBER OF SEQUENCES: 6
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: CALFEE, HALTER & GRISWOLD
    STREET: 800 SUPERIOR AVENUE
    CITY: CLEVELAND
    STATE: OHIO
    COUNTRY: USA
    ZIP: 44114
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/392,362
    FILING DATE:
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/799,138
    FILING DATE:
  ATTORNEY/AGENT INFORMATION:
    NAME: GOLRICK, MARY E
    REGISTRATION NUMBER: 34,829
    REFERENCE/DOCKET NUMBER: 22727/00139
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (216) 622-8458
    TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2134 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 127..1956
US-09-392-362-3
```

Alignment Scores:

Pred. No.:

Score:	101.50
Percent Similarity:	34.70%
Best Local Similarity:	17.48%
Query Match:	4.30%

0.021

Length:	2134	Matches:	68
		Conservative:	67
		Mismatches:	127
		Indels:	127
		Gaps:	17

DB:

US-09-807-459-2 (1-458) x US-09-392-362-3 (1-2134)

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Qy    139  ValPheAsnLeuLeuGluLysAsnValThrArgAspAlaAlaThrAspIleGluAsn  158
           |||        |||                      |||
Db    844  GTTGTGAATAGATCACAACAAGACATAAACAGAAGAATGTTGACATGATTGCTGCCGT  903

Qy    159  PheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAsp  178
           :::           |||||              |||              |||||
Db    904  AGAGAAACGTGAGTAC---TTCAATAGTACCCCTGAATATATAAACACCTTGCGAAC  954

Qy    179  GluPheGlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly  198
           |||||                                       |||
Db    955  AGAATGGGTTCCGAGCATCCGGCGAAGATG---  984

Qy    199  IleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlu  218
           |||         |||||:::|||:::|||                   |||
Db    985  CTCTCAAAGCATTTGGAGACAGTAATCAAGTCCAAAAATTCCT---GGCATTCAA  1035

Qy    219  HisSerValSerArg---  223
           |||:::
Db    1036 TCTCTAATTAACAAAACAATTGCTGAACTTGAACCTGAACTAACTCGTTTAGGAAAGCCT  1095

Qy    224  ------  230
           :::
Db    1096 GTACGAGCTGATGCTCGGGGAAAGTTGTATGCAATCATGGAAATATGCCCCTCATTTGAT  1155

Qy    231  ---TyrLysAspTyrMet-  235
           ::||||||:::
Db    1156 CAAATATTTAAAGACCATCTTGATGGCGTGCGGCCCTGGAGGTGATAAATTTATAATGTC  1215

Qy    236  --AspThrGlnIleProAlaLeuProLys---  251
           |||         |||
Db    1216 TTTGACAATCAGCTCCCCGCTCTTTAAATGAAACAGTTTGATAAGCAGCTTTCAAATG  1275

Qy    252  MetValValGlnArgLeuLeuAlaThrHrValAlaGlyTyr---  268
           :::|||:::||||||:::||||||
Db    1276 GAAAATATAAGGAAACTTATTACTGAAGGCTGAGTGGTATCAGCCTCCATCTTATAGCTCCA  1335

Qy    269  TrpTyrLysLysTrpTyrMetLysLeu---  287
           :::|||              |||:::
Db    1336 -----GAACAAGGATATCCTCGTCTAAATTGAAATCTTCTCTAAATAACT---  1377

Qy    288  ProThrLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGlyLys  307
           |||||              |||:::
Db    1378 -----ATTAGGGGCCCCGCCTGAGGCAGCCACCTGTGATGCG  1410

Qy    308  ValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyTyrGlnThrValAspPhe  327
           |||     :::                         |||
Db    1411 GTTCACTCCGCTGTTAAAGGACTTGGTTCAC---  1440

Qy    328  PheAsnLysGluIleArgAspProSerLysGlyLysAlaLeuLysGlySerAlaSerAsnAspAla  347
           |||||                          |||:::
Db    1441 -----AAAGCTATCAGTGAGACTTGGACTTGGAAGCAG---  1473

Qy    348  LysAspLeuPheGluAsnLysIleGlyTyrGlnThrValAspPheIleAsnAsnGluIle  367
           |||                               :::||
Db    1474 TATCCTGGTGTCTCCGGGTTGCAGGTTGGGCTGCTCCTGTGATTCACTA---GAAAGAAATG  1530

Qy    368  ArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPheGlu  387
           |||||                            |||
Db    1531 AGGGATGAAAAGCAAA---  1569

Qy    388  AsnLysIleGlyThrValAspPheIleAsnGluIleArgAspProSerLys  407
           ::|||               |||
Db    1570 ATGGAGGTGTGGCTATCTGACGTGTTGATTTCTTCGGAGCGTTCCTCAGATGTTGATAAG  1629
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Alignment Scores:

Pred. No.:

0.0304

Score:	100.50	Matches:	101
Percent Similarity:	35.26%	Conservative:	70
Best Local Similarity:	20.82%	Mismatches:	158
Query Match:	4.26%	Indels:	156
		Gaps:	22

Length:	2244	

DB:

US-09-807-459-2 (1-458) x US-09-272-414-1 (1-2244)

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Qy    28   TyrMetIleAsnSerArgAspMetSer---  39
           |||                                    |||     :::
Db    131  TATTATTTAATAGTGACAGCACAGTTTTAATTTTTATTTAAGTATTGCTTTAATTACCTTTAT  190

Qy    40   AlaValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCys  59
           |||:::                       |||||
Db    191  GCAATACTATTTCACACAAGAAACCGAAAAATGC---  223

Qy    60   SerAlaSerValSerAlaThrTyrMetSerArgCys-AlaLysGlnAspCysLeuThrLeuGl  79
           :::                        |||||
Db    224  -----CATAAGAGAAGAGCTAGACGTATAAAGTTCACGTGCGAACA  265

Qy    79   nSerLeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGl  99
           |||                                      :::
Db    266  ATCACATAATAAAGAAGAAGCAATAAAATATAGTCAAACATTAATTGAAAAATCCTGGTGG  325

Qy    99   nLeuGluAlaAlaPheIleLeuPheLysGluLeuSerAspAlaAsnProAlaAsnSerThrGl  119
           |||:::              |||:::||||| :::                     ::
Db    326  GTTGATGATTATAAAATAAAACATCGTCAAACAACACGGCTTCACTTTCTAATAATAAAA  385

Qy    119  uLysArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuVa  139
           :::                      |||:::|||                         |||
Db    386  GCAA-----ATGTTGAATGAAGTAGTCAACAACAACACCATTTTGACGAT---GT  430

Qy    139  lPheAsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPh  159
           |||:::|||||||:::||||||                         |||:::||
Db    431  GTTTGAT--AAAGGTAAATCTGTTACTCGAAAT---GTAACGATTAAAGAAA  478
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```
Qy   159 eAlaSerArgThrTyrLeuTyrMetAlaThrLeuThrTyrThrTyrThrAsnValAspGl  179
Db   479 GGGTCATCTCAAACATATATT---...---TTGTTAGGCTATCCACAAAAGCACAGAAG----  530

Qy   179 uPheGlyAlaSerPheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIl  199
Db   531 ----AATTGTCATTAGCAAATATTAGTGGAGTCTTT----  562

Qy   199 eLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHi  219
Db   563 ATATAAAGACTTTGAAAATCAATCGAAGATACAAAT----AA  598

Qy   219 sSerValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIl  239
Db   599 TGCTATTACGATTATCACTATAATTACGGCT  629

Qy   239 eProAlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuVal  259
Db   630 ----GTTATTTTTCTTAACAATTAC  649

Qy   259 aThrValAlaGlyThrTyrValAspThrProThrProTyrTyrLysLysTrpTyrMetLysLeuLysAs  279
Db   650 AACAGTCTTTGCGTTT----  665

Qy   279 nPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLysGlyIleArgGl  299
Db   666 -TTCTTATCGTCAAGAATTACAAAAACCTTTAAGACGTTTAAGACCAAGCTACACGTGT  724

Qy   299 uProSerLysAlaLeuGluLysValSerThrArgAspThrLysAspPheLeuPheGluAsnLy  319
Db   725 ATCTGAAGGGGATTACTCTTATAAAACCTTCTGTCACACAGAAAGAT----GA  772

Qy   319 sIleGlyGlnGlyThrValAspPhe------PheAsnLysGluIleArgAspProSerLy  337
Db   773 AATTGGTCAATTATCGGCAGGCAATTTAATCAGADTGAGTACAGAGACCACGTGTCGA  832

Qy   337 sAlaLeuLysGluLysValSerAsnAspAlaLysSerAsnLysIleIleGlyGl  357
Db   833 CGCATTA----TCCACACTCTAAAAATATTAGAGACAGCCTTAATTAACTCTATGGTAGA  886

Qy   357 nGlyThrVal------As  361
Db   887 AGGTGTCCTAGGTATTAATGAGAGTCCACAAATTATCTTATCTAATAAGATGGCGAATGA  946

Qy   361 pPheIleAsnAsnGluIleArgAspProSerLysAlaLeuLeuIleArgLysValSerThrGl  381
Db   947 TATTATGGACAATATTGATGAAGATGCTAAAACCTTTCTTATTAAGACAAATT------  998

Qy   381 yAlaGluAspLeuPheGluAsnLysIleIleGlyGlnGlyThrValAspPheIleAsnAsnGl  401
Db   999 ------GAAGATACTTTTAAATCAAAA  1027

Qy   401 uIleArgAsp----------ProSerLysAlaLeuLeuIleArgLysValSerThrGly  412
Db  1028 AATGGCTGATTTAGAAATGAATGCACGAGATTCTTGTTGCACCAAGCTATATCGATAA  1087

Qy   412 s----------ValTyrThrGluAlaAspLeuPheGluAs  423
Db  1088 GATTGAACAGGGAGGTAAAAGTGGTGTGTTCTTGACAGTTCGTGGATGACCATAATGACCA  1147

Qy   423 nLysIleGlyGlnGlyThrValAspPheIle------AsnLysGluIleArgAspPr  440
Db  1148 CAAATCTAGATCAAAATGAAGAAAGAGATTTCATTGCTATGTATCACATGAATTACGAACACC  1207

Qy   440 o-------------SerLysAlaLeuLeuIleArgLysValSerThrGluAlaAs  453
Db  1208 TATATCATTACTACAGGTTATACTGAATCAATTCAATTGTAGCATGGTATTGTTACAGAAACCGGA  1267

Qy   453 pAsnLeuGluGlu  457
Db  1268 TGAAAATAAAAGAA  1280
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RESULT 19
US-08-565-907A-1
Sequence 1, Application US/08565907A
Patent No. 5814499

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; PUBLICATION INFORMATION:   N/A
US-08-565-907A-1

Alignment Scores:

Pred. No.:
Score:                    0.11
                        100.00
Percent Similarity:      31.9%
Best Local Similarity:   20.0%
Query Match:             4.24%
DB:                         1

                                                    Length:      4467
                                                    Matches:       96
                                                    Conservative:  57
                                                    Mismatches:   121
                                                    Indels:       206
                                                    Gaps:          23

US-09-807-459-2 (1-458) x US-08-565-907A-1 (1-4467)

Qy    129  GlyLysAsnHisSerTyrPhe--------------------------------------------  135
           |||||||||||:|||:||:
Db   1411  GGAAAATCAGATTCTTTTATTTTAAAAGTATTAATATGGAATCCTTTGCAGATTATTTA-----  1470

Qy    136  -----HisAspLeuValPheAsnLeuLeuGluLys--------------------------------  145
                ||||||||||||||::|
Db   1471  AGGAGTCATCATGTTTAAAAACACATTTTACGGTAAAAACCTCTATCACACAGACCCAGTA      1530

Qy    146  -----AsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr-------  163
                ||||:||    :::||       |||
Db   1531  TATTTTAATATTCCAAAAAAAATATAGAAGCTAGAAGACAATATATAAGATGCCCAATTATAC    1590

Qy    164  LeuTyrMetAlaThrLeuTyrTyr-----------------------------------------  177
           ||||||||                 ::|   LysThrTyrThrAsnVal---
Db   1591  AGTTATATGGCCATTAAATTATTATATGTCAAATAAAAAAGAGTTTATAGAAGTATTT        1650

Qy    178  ----AspGluPheGlyAlaSer-----PhePheAsnLysLeuSerPhe------------------  190
                ::|                    |||:||||||||||||||
Db   1651  ATTGATAACAAAATTTTCAACGTCAAAATTTTTAATCAATTTGAATTTTGATTATCCTAAG    1710

Qy    191  -----------------------ThrThrGlyLeuPheGlyTrpGlyIleLeuSerArgAlaLeuLysGln  205
                                   |||      |||||||||||:::
Db   1711  ACACAAGAGAATTACACAAACATTATTATATGGA----GGAATAAAAGAAA              1755

Qy    206  IleIleArgSerAsnLeuProLeuAspIleGlyThr----------------GluHis  219
           |||||||||||    |||||||:::
Db   1756  --------TTACATTTAGATTTATCTAATTTTATCATACTTTATTATACACAT        1800

Qy    220  SerVal------------------------SerArgLeuGlnHisIleThrSerSerTyr   231
           ||||||                        ::|
Db   1801  AGTATACCATGGATCATTGATGGAAAATCTGCACTCTAAACAAAAATGAAAAAAGGGTTT    1860

Qy    232  LysAspThrMetAspThrGlnIleProAlaLeuProLysPhe-AlaLysArgPheSerLe      251
           :::    |||                              |||
Db   1861  TCTAATACACATTAGATACTTTGATTACACAGCTTGT--CAATACGACGAAAACACATGGCATT   1917

Qy    251  uMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrProTrpTyrLy      271
                      |||                    ::|
Db   1918  CCAACTGGAAAATCTATTGTCTAGGAATTATACCGAACTATATATGTGCCATTTGATAAA   1977

Qy    271  sLysTrp----------------------------------------------------------  273
           |||||||
Db   1978  CAAATGGAATAATAAGAAGTTTGTGTATTCAAGATATGTAGATGATTTTATATTTCCGTTT  2037

Qy    274  ------TyrMetLysLeuLysAsnPhe--------------------------------------  280
                 |||||||
Db   2038  ACTTTTGACAATGAAAAGCAAAGAATTTTTAAAATGAAATTTAAATCTAATCTGTCGAGAAAAT  2097

Qy    281  ----------------------------------------------IleProThrLysLy------  291
                                                          |||||||||||
Db   2098  AACTTAATTAATTAATTAATGATAATAAAAACGAAAGTTGACAATTTCCCGTTTGTTGATAAATCG  2157

Qy    281  tValAsnArgValPhe-----------------------------------------------  291
           |||||||||||||:::||
Db   2158  AGTAAATCGGATATTTTTTCTTTTTTGAAAATATTACTTCAACTAATTCCAACGAC-AA  2216

Qy    291  sPhePheAsnLysGluIleArgGlu----------------------------------------  299
           ::::|||||||||||
Db   2217  GTTGGATT--AAAGAAATAAGCAATTTTATAGATATTTATTGTGTGAATGAGAAACATTTAGG  2273

Qy    300  ------------------------------------------ProSerLysAlaLeuLysGluLysVa  308
                                                       ::||||||||:|||
Db   2274  GAATAAGGAGGCTATAAAAGTGTATTTTCCCAGTATTATAACAAATTACATTGAAACAAAAA--  2331

Qy    308  1SerThrAspThrLysAspLeu------------------------------------------  315
           ||||||||||||||::::||
Db   2332  -AAAGTAGATACTAAAAAATATAGACAATATCTTTTCGAAAAGAAAACATGGTTACCAATTT   2390

Qy    315  --------------------------------------------------------------  315
Db   2391  TAATGTTTTTCGAAAAATATTATACATTTATTCATTAAAAAGATTCAAGATTAACTAATAAGTT   2450

Qy    316  -------PheGlu--------AsnLysIleGlyGlnGlyThrValAspPhePhePheAsn--    329
                  :|||||        :::||
Db   2451  TTTGACTTTCTTTGGAAAATATTAATGAATTTGGATTTGTCAAGTTTATCAGCTTCAAATAT    2510

Qy    330  ------LysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAl  347
                 ||||||||||||||||||||||||||||||||
Db   2511  TGTAAAAAAAATATTTAGTAATAATTACAAAGGGCTTAAAAGAAAAAATAGACCTATCG   2570

Qy    347  aLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhePheAsnAsnGluI1  367
           ||||||||::::||
Db   2571  TAAAAAAATAATTTTTAATCAAGAATATATCAAAATATTGTTGTATATGGTTGTCTTTTGAAT  2630

Qy    367  eArgAsp------------ProSerLysAlaLeuIleArgLysValSerThrGlyIleAlaGluAspIle  385
           |||||||            ::|||
Db   2631  AGATGATTTATTAAAATCAAGAGAAGAATTACTAAACTTAATTGATTTAAATATTGGATTA  2690

Qy    385  uPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspPr  405
           |||||||||:::||
Db   2691  T-------TCTTTAATTTAGGGACGACCGCATTTTATACCTAAAGAAT---------  2727

Qy    405  oSerLysAlaLeuIleArgLysValTyrThrGlyValAlaAspAspLeuPheGluAsn    423
           ::||||    :::
Db   2728  -AGTTCATAATAAAATTGGAAAAAATTATTTAAAAAAAATAGATCAATTATTATTTTAAT    2781
```

```
;  REFERENCE/DOCKET NUMBER: Quest 4.1-158
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (517) 347-4100
;     TELEFAX: (517) 347-4103
;     TELEX: No. 5910571e
;  INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 4467
;        TYPE: Nucleotide
;        STRANDEDNESS: Single
;        TOPOLOGY: Linear
;     MOLECULE TYPE:
;        DESCRIPTION: Genomic DNA
;     HYPOTHETICAL: No
;     ANTI-SENSE: No
;     FRAGMENT TYPE: N/A
;     ORIGINAL SOURCE:
;        ORGANISM: Lactococcus lactis
;        STRAIN:
;        INDIVIDUAL ISOLATE: W1
;        DEVELOPMENTAL STAGE: N/A
;        HAPLOTYPE: N/A
;        TISSUE TYPE: N/A
;        CELL TYPE: bacterium
;        CELL LINE: N/A
;        ORGANELLE: N/A
;     IMMEDIATE SOURCE:
;        LIBRARY: genomic
;        CLONE: SMQ-20
;     POSITION IN GENOME: N/A
;     FEATURE:
;        NAME/KEY: phage abortive infection
;        LOCATION: N/A
;        IDENTIFICATION METHOD: sequencing
;        OTHER INFORMATION: DNA encoding phage
;        OTHER INFORMATION: resistance
;     PUBLICATION INFORMATION: N/A
US-08-910-551B-1

Alignment Scores:
  Pred. No.:
  Score:              0.11
  Percent Similarity: 100.00
  Best Local Similarity: 31.94%
                      20.04%
  Query Match:        4.24%
  DB:                 2

US-09-807-459-2 (1-458) x US-08-910-551B-1 (1-4467)

Qy    129 GlyLysAsnHisSerTyrPhe------------------------------------------------ 135
          ||||||||||:::|
Db   1411 GGAAAATCAGATTCTTTTATTTTAAGTAGTATTTAATATGGAATCCTTTGCAGATTATTTA 1470

Qy    136 ------HisAspLeuValPheAsnLeuGluLys---------------------------- 145
          ||||||||||||
Db   1471 AGGAGTCATGATTAAAAACACATTTAACGGTAAAAAACCTCTACAACAGACCCAGTA 1530

Qy    146 -----AsnValThrArgAspAlaAspAlaThrAspAspIleGluAsnPheAlaSerArgTyr 163
          ||:|
Db   1531 TATTTTAATATTCCAAAAAAATATAGAAGCTAGAAGACAATAATAAGATCCCCAATTTATAC 1590

Qy    164 LeuTyrMetAlaThrLeuThrTyr------------------------------LysThrTyrThrAsnVal-- 177
          ||||||||||              |||                            :::
Db   1591 AGTTATATGGCATTAAATTATATATGTGCAATAAAAAAGAGTTTTATAGAAGTATTT 1650

Qy    178 -----AspGluPheGlyAlaSer---PhePheAsnLysSerPhe---------------- 190
          |||||||||:||
Db   1651 ATTGATAACAAATTTCAACGTCAAAATTTTTTAATCAATTGAATTTTGATTATCCTAAG 1710

Qy    191 ------------ThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeuLysGln 205
          |||
Db   1711 ACACAAGAAAATTACACAAACATTATTATATATGGA---GGAATAAAGAAA 1755
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```
Qy    206 IleIleArgSerAsnLeuProLeuAspIleGlyThr------------------------GluHis 219
          |||                                                        |||
Db   1756 ------------------------TTACATTTAGATTTATCTAATTTTTATCATACTTTTATATACACAT 1800

Qy    220 SerVal------------------------------SerArgLeuGlnHisIleThrSerSerTyr 231
          |||:::                               :::
Db   1801 AGTATACCAATGGATGATGATTGAATGGGAAAATCTGCATCTAAACAAAATTAGAAAAAAAGGGTTT 1860

Qy    232 LysAspTyrMetAspThrGlnIleProAlaLeuProLysPhe-AlaLysArgPheSerIle 251
          |||::                                    :::
Db   1861 TCTAATACATTAGATACTTTTGATTACAGACTTGT---CAAATACGACGAAAACACTGGCATT 1917

Qy    251 uMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrProTrpTyrLy 271
          |||||||                          |||:::
Db   1918 CCAACTGGAAAATCTATTGTCTAGGATTATTACCGAACTATATATGTGCCAATTTGATAAA 1977

Qy    271 sLysTrp--------------------------------------------------Me 281
          ||||||
Db   1978 CAAATGGAATATATAGAAGTTTGTGTTATTCAAGATATAGTAGATGATTTTATATTTCCGTTT 2037

Qy    274 ------TyrMetLysLeuLysAspLeu---------------------- 280
          ||||||
Db   2038 ACTTTTGAGAATGAAAAGCAGAGAATTTTAAATGAATTCGATCTCTCGAGAAAAT 2097

Qy    281 tValAsnArgValPhe--------------------------IleProThrLysLy 291
          |||||||||:::|||                            ||
Db   2098 AACTTAATTATTAATGAATAATAAAACGAAAGTTGACAATTTCCCGTTGTTTGATAAATCG 2157

Qy    291 sPhePheAsnLysGluIleArgGlu----------------------------------- 299
          |||||||||
Db   2158 AGTAAAATCGGATATATTTTTTCTTTTTTTGAAAAATATTACTTCAACTAATTCCAACGAC-AA 2216

Qy    300 ------------------------------ProSerLysAlaLeuLeuLysGluLysVa 308
                                        ||||||||:::||
Db   2217 GTGGATT---AAAGAAAATAAGCAATTTATTATAGATTATTGTGTGATGAGAACATTTAGG 2273

Qy    308 lAsnLysIleGlyGlyThrValAspPhePheAsn-- 329
          |||||||:::                |||
Db   2274 GAATAAGGAGGCTATAAAAATGTATTTTCCCAGTTATAACAAATACATTGAAACAAAA- 2331

Qy    308 lSerThrAspThrLysAspLeu----------------------------- 315
          |||||||||
Db   2332 -AAAGTAGATACTAAAAAATATAGACAATATCTTTCGAAAAGAACACATGGTTACCAATTT 2390

Qy    316 ----------------PheGlu------AsnLysIleGlyGlyThrValAspPheAsn-- 329
                          ||||||      :::
Db   2391 TAATCGTTTCGAAAAAATATTAGATTTATCATTAAAAGATTCAAGATTAACTAATAAGTT 2450

Qy    330 --------------LysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAl 347
                        |||
Db   2451 TTTGACTTTCTTTGAAAATATTCAAGATTTCAGCTTCAAATAT 2510

Qy    347 aLysAspLeuProPheGluAsnLysIleGlyGlyThrValAspPheIleAsnAsnGlull 367
          ||||:||                                        :::
Db   2511 TGTAAAAAAATAATTTTAGTAATAAAGGGCCTTAAAAGAAAAAAATAGACCACTATCG 2570

Qy    367 eArgAsp--------ProSerLysAlaLeuIleLeuArgLysValSerThrGlyAlaGluLe 385
          |||:::
Db   2571 TAAAAATAATTTAATCAAGAATATATCAAATATTGTGTATAGGTTGTCTTTGAAAT 2630

Qy    385 uPheGluAsnLysIleGlyThrValAspPheIleAsnAsnGluIleArgAspPr 405
          ||||||:::
Db   2631 AGATGATTTATTAAATCAACAGAAGAATTACTAAACTTAAATGCTTTAAATATTGATGATTA 2690

Qy    405 oSerLysAlaLeuIleLeuArgLysValTyrThrGlnLeuAspAspLeuPheGluAsn 423
          |||||||                                        |||
Db   2691 T----TCTTTAATTTAGGGACGAGATTTTATACCTAAAGAAT----- 2727

Qy    191 --------ThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeuLysGln 205
          |||
Db   2728 -AGTTCATATAAAATTGGAAAAATTAATAAAAAATTATTAATAAGATCAAATTATTATTAAT 2781
```

```
US-08-909-425A-1
Patent NO. 5928688
GENERAL INFORMATION:
  APPLICANT:
  APPLICANT:  Sylvain Molneau, Barbara
  APPLICANT:  J. Holler, Peter A. Vandenbergh,
  APPLICANT:  Ebenezer R. Vedanthu, Jeffrey K.
  APPLICANT:  Kondo
  TITLE OF INVENTION:  DNA Encoding Phage
  TITLE OF INVENTION:  Abortive Infection Protein
  TITLE OF INVENTION:  From Lactococcus
  TITLE OF INVENTION:  lactis, and Method of Use Thereof
  NUMBER OF SEQUENCES:  1
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  Ian C. McLeod
    STREET:  2190 Commons Parkway
    CITY:  Okemos
    STATE:  Michigan
    COUNTRY:  USA
    ZIP:  48864
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Diskette 5.25 inch,
    MEDIUM TYPE:  360 Kb storage
    COMPUTER:  Acer
    OPERATING SYSTEM:  MS-DOS (version 4)
    SOFTWARE:  Wordperfect 5.1
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/909,425A
    FILING DATE:  August 11, 1997
    CLASSIFICATION:  435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  08/565,907
    FILING DATE:  December 1, 1995
  ATTORNEY/AGENT INFORMATION:
    NAME:  Ian C. McLeod
    REGISTRATION NUMBER:  20,931
    REFERENCE/DOCKET NUMBER:
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (517) 347-4100
    TELEFAX:  (517) 347-4103
    TELEX:  NO. 5928688e
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  4467
    TYPE:  Nucleotide
    STRANDEDNESS:  Single
    TOPOLOGY:  Linear
  MOLECULE TYPE:
    DESCRIPTION:  Genomic DNA
  HYPOTHETICAL:  No
  ANTI-SENSE:  NO
  FRAGMENT TYPE:  N/A
  ORIGINAL SOURCE:
    ORGANISM:  Lactococcus lactis
    STRAIN:
    INDIVIDUAL ISOLATE:  W1
    DEVELOPMENTAL STAGE:  N/A
    HAPLOTYPE:  N/A
    TISSUE TYPE:  N/A
    CELL TYPE:  bacterium
    CELL LINE:  N/A
    ORGANELLE:  N/A
  IMMEDIATE SOURCE:
    LIBRARY:  genomic
    CLONE:  SMQ-20
  POSITION IN GENOME:  N/A
  FEATURE:
    NAME/KEY:  phage abortive infection
    LOCATION:  N/A
    IDENTIFICATION METHOD:  sequencing
    OTHER INFORMATION:  DNA encoding phage
    OTHER INFORMATION:  resistance
  PUBLICATION INFORMATION:  N/A
```

```
US-08-909-425A-1

Alignment Scores:
Pred. No.:
Score:                    0.11
Percent Similarity:     100.00    Length:         4467
Percent Identity:        31.94%   Matches:          96
Best Local Similarity:   20.04%   Conservative:     57
Query Match:              4.24%   Mismatches:      121
DB:                          2    Indels:          206
                                  Gaps:             23

US-09-807-459-2 (1-458) x US-08-909-425A-1 (1-4467)

Qy   129 GlyLysAsnHisSerTyrPhe-------------------------------------  135
         ||||||:||:::  ||:|::::
Db  1411 GGAAAATCAGATTCTTTTTATTTTAAAGTATTAATATGGAATCCTTTGCAGATTATTTA  1470

Qy   136 ------HisAspLeuValPheAsnLeuLeuGlyLys---------------------  145
               |||||||||            :::            |||
Db  1471 AGGAGTCATGATTTAAAAAACACATTTTAACGGTAAAAAACCTCTATCAAACAGACCCAGTA  1530

Qy   146 ------AsnValThrArgAspAlaAspAlaThrArgAspIleGluAsnPheAlaSerArgTyr  163
               ||:||   ||||||:::::||:|||::||
Db  1531 TATTTTAATTATTCCAAAAAAATATAAGAAGCTAGAAGACAATATAAGATGCCCAATTTATAC  1590

Qy   164 LeuTyrMetAlaThrLeuTyrTyr--------------------- LysThrTyrThrAsnVal---  177
         ||||||||||          :::                     |||     |||
Db  1591 AGTTATATGGCATTAAATATTATTATAATGTGACAATAAAAAGAGAGTTTTATAGGAAGTATTT  1650

Qy   178 -----AspGluPheGlyAlaSer---PhePheAsnLysLeuSerPhe-----------  190
              |||         ||| |||||||||::|||:::|||::|||
Db  1651 ATTGATTAACAAAATTTCAAACGTCAAAAATTTTTTTAAATCAAATTGAATTTTGATTATCCTAAG  1710

Qy   191 ----------ThrThrGlyLeuPheGlyThrGlyIleLeuTyrArgAlaLeuLeuLysGln  205
                      ||| |||::|||     |||||||:|:::
Db  1711 ACACAACAAGAAATTACACAAAACTATTATTATATGA---GGAATAAAGAAA-------  1755

Qy   206 IleIleArgSerAsnLeuProLeuAspIleGlyThr-------------------GluHis  219
         |||      ||||||:::       |||                          |||
Db  1756 TTACATTTAGATTTATTCTAATTTATCATACTTTATATATACACAT  1800

Qy   220 SerVal-----------------------SerArgLeuGlnHisIleThrSerSerTyr  231
         ::::                         ::                       :::
Db  1801 AGTATACCATGGATGATGATTGCATGGAAAAATCTGCATCTAAACATAATAGGAAAAAAGGGTTT  1860

Qy   232 LysAspThrTyrMetAspThrGlnIleProAlaLeuProLysPhe-AlaLysArgPheSerIle  251
                 |||      ||||||||      :::|||        ::::||       |||
Db  1861 TCTAATCACATTAGATACTTTGATTACAGCCTTGT--CAATACGACGAAAACACATGGCATT  1917

Qy   251 uMetValValGlnArgLeuLeuAlaThrHisValIleAlaGlyThrTyrValAspThrProTrpTyrLy  271
               :::                |||             :::|||
Db  1918 CCAACTGGAAATCTATTGTCTAGGATTATTACCGAACTATATATATGTGCCCATTTTGATTAA  1977

Qy   271 sLysTrp------------------------------------------------  273
         ||:|||
Db  1978 CAAATGGAATATATAGAAGTTTGTTGTATTCAAGATATAGTTGAGATGATTTATTATTCCGTTT  2037

Qy   274 ------TyrMetLysLeuLysAsnPhe------------------------------  280
               ||||||          ||||||||
Db  2038 ACTTTTGAGAATGAAAAAGCCAAGAATTTTTAAATGAAATTTAAATCTAAACTGTGTGGAGAAAAT  2097

Qy   281 -------------------------------------------------------Me  281
                                                               |||
Db  2098 AACTTAATTATTAATGATAATAAAAACGAAAAGTTGACAAATTTCCCGTTTGTTGTTGATAAATCG  2157

Qy   281 tValAsnArgValPhe----------------------------IleProThrLysLy  291
         ||:|||||||||:::||                          ||:|||||:|:|
Db  2158 AGTAAATCGGATATTTTTTTTTCTTTTTTTGAAAATATTACTTCAACTAATTCCAACGAC--AA  2216

Qy   281 sPhePheAsnLysGluIleArgGlu----------------------------  299
         |:||||||||||||                                     |:|
Db  2217 GTGGATT---AAAGAAAATAAGCAAATTTTATAGATTATTGTGTCAATGAAGAACATTAGG  2273

Qy   300 -------------------------------------ProSerLysAlaLeuLysGluLysVa  308
```

RESULT 22
US-08-229-781-27
Sequence 27, Application US/08229781
Patent No. 5589174

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.

TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
    ADDRESSEE: Wenderoth, Lind & Ponack
    STREET: 805 Fifteenth Street, N.W., #700
    CITY: Washington
    STATE: D.C.
    COUNTRY: U.S.A.
    ZIP: 20005

COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: MS-DOS
    SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/229,781
    FILING DATE: April 19, 1994
    CLASSIFICATION: 530

PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/054,016
    FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
    NAME: Warren M. Cheek, Jr.
    REGISTRATION NUMBER: 33,367
    REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202-371-8850
    TELEFAX:
    TELEX:

INFORMATION FOR SEQ ID NO: 27 :
SEQUENCE CHARACTERISTICS:
    LENGTH: 1754 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    MOLECULE TYPE: cDNA to genomic RNA
    HYPOTHETICAL:
    ANTI-SENSE:
    FRAGMENT TYPE:
ORIGINAL SOURCE:
    ORGANISM: A/Suita/1/89
    STRAIN:
    INDIVIDUAL ISOLATE:
    DEVELOPMENTAL STAGE:
    HAPLOTYPE:
    TISSUE TYPE:
    CELL TYPE:
    CELL LINE:
    ORGANELLE:
IMMEDIATE SOURCE:
    LIBRARY:
    CLONE:
POSITION IN GENOME:
    CHROMOSOME/SEGMENT:
    MAP POSITION:
    UNITS:
FEATURE:
    NAME/KEY:
    LOCATION:
    IDENTIFICATION METHOD:
    OTHER INFORMATION:
PUBLICATION INFORMATION:
    AUTHORS:
    TITLE:
    JOURNAL:
    VOLUME:
    ISSUE:
    PAGES:
    DATE:
    DOCUMENT NUMBER:
    FILING DATE:
    PUBLICATION DATE:
    RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-27

Alignment Scores:
Pred. No. :   0.0269   Length: 1754
Score: 99.50   Matches: 58
Percent Similarity: 35.32%   Conservative: 37
Best Local Similarity: 21.56%   Mismatches: 89
Query Match: 4.22%   Indels: 85
                     1   Gaps: 13
DB:

US-09-807-459-2 (1-458) x US-08-229-781-27 (1-1754)

Qy   195 PheGlyTrpGlyIleLysArgAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAsp 214
           | | | | | : | | | | | | | : : | |
Db   852 TTTGGGTCAGGA---------------------------ATCATCACCTCAAACGCATCAATGGAT 890

Qy   215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSerSer------TyrLys 232
           | | | | : : : | | : : : :
Db   891 GAATGTGACGCGGAAGTGTCAAACACCCAGGGAGCTATAAACAGTAGTCTTCCTTTCCAG 950

Qy   233 AspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMet 252
           | | | | | : : :   : : :
Db   951 AATGTACACCCAGTCACAATAGGAGAGAGTGTCCAAAGTATGTCAGGAGTACAAAATTAAGG 1010

Qy   253 ValVal------------------------------------GlnArgLeuLeuAlaThrVal 261
           | | : : :   : : :
Db   1011 ATGGTTACAGGACTAAGGAACATCCCATCCATTCAATCCAGAGGTTTGTTTGGAGCCATT 1070

Qy   262 AlaGlyTyrValAspThrProTrp---------TyrLysLysTrpTyr--------- 274
           | | | | | : : : : : : | | | | |
Db   1071 GCCGGTTCATTGAAGGGGGGTGGACTGGAATGATAGATGGTATGGTTATCATCAT 1130

Db   2274 GAATAAGGAGGCTATAAAAGTATATTTCCCAGTTGTTATTAACAAATACATTGAAACAAAA-- 2331
                                                           : : : | | | : : : | | |
Qy   308 1SerThrAspThrLysAspLeu--- 315
           | | | | | | | | | : : : | | |
Db   2332 -AAAGTAGAATACTAAAAATATAGACAAATATCTTTTCGAAAAGAAGAAACATGGTTACCAATTT 2390

Qy   315 --- 315
Db   2391 TAATGTTTTCGAAAAATATTAGATTTATCATTAAAAGATTCAAGATTAACTAATAAGTT 2450

Qy   316 ----------------------PheGlu-----AsnLysIleGlyGlyThrValAspPhePheAsn-- 329
                                  | | | : : : | | : : :
Db   2451 TTTGACTTTCTTTGAAAATATTAATGAATTTGGATTTTCAAGTTTATCAGCTTCAAATAT 2510

Qy   330 -----------------LysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspPAl 347
                            | | | | | | | | | | | | | : : :
Db   2511 TGTAAAAAATATTTTAGTAATAATTCAAAAGGCCTTAAAAGAAAAAATAGACCACTATCG 2570

Qy   347 alLysAspAspLeuPheGluAsnLysIleGlyGlyThrValAspPheLeuAsnLysValIleLeu 367
           | | | | | : : : | | |
Db   2571 TAAAAATAAATTTTAATCAAGAATTATATCAAAATAGTTGTATATGGTTGTGTCTTTGAAAT 2630

Qy   367 euArgAsp--------ProSerLysAlaLeuIleLeuLysGluLysIleAlaLysLeuGluArgAspPr 385
           | | | | | | : : :
Db   2631 AGATGTTTATTAAATCAAGAAGAATTACTAAACTTAATTGATTTAAATATTGATGATTA 2690

Qy   385 uPheGluAsnLysIleGluGlyGlyThrValAspPheIleAsnAsnGluIleArgAspPr 405
           | | | : : : : : | | |
Db   2691 T---------TCTTTAATTTAGGGACGGATTTTATACCTAAAGAAT-------------- 2727

Qy   405 oSerLysAlaLeuIleArgLysValTyrThrGluAlaAspLeuPheGluAsn 423
           : : : | | | | | | | |
Db   2728 -AGTTCATATAAAATTGGAAAAATTATTAAAAAAAATTAGATCAAATTATTTATTTAAT 2781

us-09-807-459-2.rni

TELEX:
INFORMATION FOR SEQ ID NO: 27 :
SEQUENCE CHARACTERISTICS:
  LENGTH: 1754 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
  ORGANISM: A/Suita/1/89
US-08-630-918-27

Alignment Scores:
Pred. No.:
Score: 0.0269
Percent Similarity: 99.50
Best Local Similarity: 35.32%
Query Match: 21.56%
DB: 4.22%

	Length:	1754
	Matches:	58
	Conservative:	37
	Mismatches:	89
	Indels:	85
	Gaps:	13

us-09-807-459-2 (1-458) x us-08-630-918-27 (1-1754)

APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Wenderoth, Lind & Ponack
  STREET: 805 Fifteenth Street, N.W., #700
  CITY: Washington
  STATE: D.C.
  COUNTRY: U.S.A.
  ZIP: 20005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: MS-DOS
  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/630,918
  FILING DATE: April 5, 1996
  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/229,781
  FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/054,016
  FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
  NAME: Warren M. Cheek, Jr.
  REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-371-8850
  TELEFAX:

RESULT 23
US-08-630-918-27
Sequence 27, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:

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Qy    393 GlyThrValAspPheIleAsnAsnGlu 401
              :::|||  |||  :::
Db   1563 GAAAAAATTGATGGAGTGAAATTGGAA 1589
```

RESULT 24
US-09-004-422-27
Sequence 27, Application US/09004422

Patent No. 6337070

GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 27 :
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Suita/1/89
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:

UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-09-004-422-27

US-09-807-459-2 (1-458) x US-09-004-422-27 (1-1754)

Alignment Scores:
Pred. No. :
Score: 0.0269   Length: 1754
Percent Similarity: 99.50   Matches: 58
Percent Similarity: 35.32%   Conservative: 37
Best Local Similarity: 21.56%   Mismatches: 89
Query Match: 4.22%   Indels: 85
DB: Gaps: 13
```

```
Qy   195 PheGlyTrpGlyIleLysArgAlaLeuLysGlnIleIleGluArgSerAsnLeuProLeuAsp 214
             |||||||||:||  ||  :::  |||| |||
Db   852 TTTGGGTCAGGA----------------ATCATCACCCTCAAACGCCATCAATGGAT 890

Qy   215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSerSer------TyrLys 232
             :::       ||||||| |||||| :::||
Db   891 GAATGTGACGCGAAGTGTCAAACACCCCAGGGAGGCTATAAACAGTAGTCGTTCCTTTTCCAG 950

Qy   233 AspTyrMetAspThrGlnIleProIleAlaLeuProLysPheAlaLysArgPheSerLeuMet 252
             ||||||:|::: :::
Db   951 AATGTACACCCAGTCACAATAGGAGAGTCTCCAAAGTATGTCACGGAGTACAAAATTAAGG 1010

Qy   253 ValVal------------------GlnArgLeuLeuAlaThrVal 261
             ::|||                    :::   |||
Db  1011 ATGGTTACAGGACTAAGGAACAATCCCATCCATTCAAATCCAGAGGTTTGTTTGGAGCCATT 1070

Qy   262 AlaGlyTyrValAspThrProTrp------------TyrLysLysTrpTyr---------- 274
             ||||||  :::|||                |||
Db  1071 GCCGGTTTCATTGAAGGGGGTGGACTGGAATGGAATGGTTATGGTTATCATCAT 1130

Qy   275 ------------------------------MetLysLeuLysAsn 279
                                          |||
Db  1131 CAGAATGAACAAGGAATCTGGCTATGCTCGGGATCAAAAAGCACACAAAATGCCATTAAC 1190

Qy   280 PheMetValAsnArgVal-------------------PheIleProThr 289
             ::|  |||  :::|||                       |||
Db  1191 GGAATTACAAACAAGGTGAATTCTGTAAATCGAGAAAATGAACACTCAATTCACAGCTGTG 1250

Qy   290 LysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysLysValSer 309
             |||  ||||||||     :::    :::||||||
Db  1251 GGCAAAGAATTCAACAAA---TTAGAAAGAAGGAGAATACTTAAATAAAAAAGTTGAT 1307

Qy   310 ThrAspThrLysAsp------------------LeuPheGluAsnLys 319
             |||                                |||
Db  1308 GATGGATTTCTGGACATTTGGACATATAATGCAGAATTGTTTGGTTCTACTGGAAAAT--- 1364

Qy   320 IleGlyLyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeu 339
             :::|||||       :::      :::
Db  1365 -----GAAAGGACTGTTGGATTTCATGACTCAAAATGTGAAGAATCGTGTATGAGAAAGTA 1418

Qy   340 LysGluLysLysValSerAsnAspAlaLysPheGluAsnLysIleLysGlyGlyThr 359
             |||  :::||||||||||||||  :::||
Db  1419 AAAAGCCAATTAAAGAAAAATAATGCCAAAGAA--------ATAGGATACGGGTGT 1463
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RESULT 25
US-09-308-375-1
Sequence 1, Application US/09308375
Patent No. 6300117
GENERAL INFORMATION:
 APPLICANT: Genencor International, Inc.
 TITLE OF INVENTION: Proteases From Gram-Positive Organisms
 FILE REFERENCE: GC394-PCT
 CURRENT APPLICATION NUMBER: US/09/308,375
 CURRENT FILING DATE: 1999-05-14
 EARLIER APPLICATION NUMBER: EP9719636.4
 EARLIER FILING DATE: 1997-09-15
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 7100
 TYPE: DNA
 ORGANISM: Bacillus subtilis
US-09-308-375-1

US-09-807-459-2 (1-458) x US-09-308-375-1 (1-7100)

Alignment Scores:
Pred. No.:
Score:                    0.315
Percent Similarity:      99.00          Length:         7100
Best Local Similarity:   43.61%         Matches:          66
Query Match:             21.64%         Conservative:     67
DB:                       4.20%         Mismatches:      128
                                        Indels:           45
                                        Gaps:             14
```

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Qy  360  ValAspPhe--------IleAsnAsnGlnIleArgAspProSerLysAlaLeuIleArg 376
              :::|||                    ||||
Db 1464  TTTGAATTCTACCACAAGTGTAACAATGAA-----------TGCAATGGAA 1502

Qy  377  LysValSerThrGlyAlaGluAspLeu--------PheGluAsnLysIleGlyGln 392
Db 1503  AGTGTGAAAAATGGAACTTATGACTATCCAAAATATTCCGAGGAATCAAAGTTAAACAG 1562

Qy  393  GlyThrValAspPhePheIleAsnAsnGlu 401
              |||
Db 1563  GGAAAAATTGATGGAGTGAAAATTGGAA 1589
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```
Qy  188  LeuSerPheThrThrGlyLeuPheGlyTrpGlyTyrLeuLysArgAlaAlaLeuLysGlnIleIle 207
              ::|||  |||  ||| |||| | ||||
Db 5585  GTGAGCTACAGAAACAACTTGTTCAATCTAAAGTTGATGAGACACTTAAGTCAA---TTG 5641

Qy  208  ArgSerAsnLeuProLeuAspIleGlyThrGlnHisSerValSerArgLeuGlnHisIle 227
Db 5642  AAAAGTCATCTTCT-AAAACCCAAGGGAAAAATTAAAGATGTCGATAACAAAATTCAATG 5700

Qy  228  ThrSerSerTyrLysAsp--------TyrMetAspThrGlnIleProAlaLeu------ 242
              |||                |||          ||||
Db 5701  ACTGAAGAAGATGAAGACAAAGGTTAAATACTATAGCAACGACAAAATAAAGCTCATTCAACAA 5760

Qy  243  ---ProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrVal 261
              ||    |||          :::|||    :::|||          ||| |||
Db 5761  CAACAAAAGGACGAAGAAAATACATTAAGCACGTTGAAGAACAAAAGAAAGCT---GCG 5817

Qy  262  AlaGlyTyrValAsp--------ThrProThrPTyrLysLysTrpTyrMetLys 276
              :::|||                   ||| |||
Db 5818  AAAGGTTTCCCTGACATCCAGGAACAGATCACTCAAGAAATGCAAAACTGGAAAGATAAA 5877

Qy  277  LeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLysGlu 296
              ||||||||                            |||||
Db 5878  CAGAAAGATTTT-----AACCTTGAGCTTTATAAACACCAAG 5919

Qy  297  IleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLysAspPhe 316
              ||||:::|||          ||||||  |||:::||
Db 5920  ATCAAGGAGATATCTATAAATCATTGGCTGATGAAGTTGTATCATCTACACAAGAGATGTAC 5979

Qy  317  Glu--------AsnLysIleGlyGlnGlyThrValAsp 326
              |||                   |||  :::|||
Db 5980  GAAAAAAATGGGTGATATTGAGTTAGAAGCGCCATCAGAAAAGCGACTCAAGAGACTTGATCGAT 6039
```

```
Qy  327  PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGlu-----LysValSerAsn 345
              ::|||                               |||||        ||||
Db 6040  GAGATAGACAAG-----ACTGATGACGAGGCTAAATTTCAAAAGAATTAAAAAAGAACAA 6096

Qy  346  AspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp-------Phe 362
              |||                               :::||              |||
Db 6097  GACACTATTCAAAAGTTGACTGACCAAAAATTAATCAATACTCTCTTGATGATTC 6156

Qy  363  IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAla 382
              ::||                                ||||
Db 6157  GGAAAGTCAAAAGTCAAAAGAACTAACTGAACAGCTT--CAAAAAGAGCAGTTAGACCTT 6213

Qy  383  GluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhePheIleAsnAsnGluIle 402
              ||||              :::||                            :::|||
Db 6214  GATGATTTTCAAAAGGATCGGGAAAGTAACAAAACGGAAAAGCGCTCCAAGAGATCAGCTC 6273

Qy  403  ArgAspProSerLysAlaLeuIleArgLysValTyrThrGluAlaAspAsp-------- 419
              |||                     ||||
Db 6274  GAAAAAAGATGAGGAGTCAATCAACAATAAATACGGATAATCTTGTAAATGATGAACGAGCC 6333

Qy  420  -----LeuPheGluAsnLysIleGlyGlnGlyThrValAspPhePheIleAsnLysGluIle 437
              ||        :::|||          |||           |||
Db 6334  TTTAAAAAGCTTGAGGATAAGATTATGAATGGAAAAAATCACCGATATCGGCTAAGCAGCTT 6393

Qy  438  ArgAspProSerLysAlaLeuIleArgLysVal-----------SerThrGluAlaAsp 453
              |||                     :::|||              :::|||
Db 6394  AATGACTTTTCTAAGTTTATTAATACCAATATGGGAGTCCATTGAAAAAGTATTTTCAAAC 6453

Qy  454  AsnLeuLeuGluLys 458
              |||||:::|||
Db 6454  AACCTGATTGATAAA 6468
```

```
RESULT 26
US-08-743-637B-169
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: PICARD, Francois J.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
 TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
 TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
 TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: QUARLES & BRADY
  STREET: 411 EAST WISCONSIN AVENUE
  CITY: MILWAUKEE
  STATE: WISCONSIN
  COUNTRY: USA
  ZIP: 53202-4497
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/743,637B
  FILING DATE: 04-NOV-1996
  CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/526,840
  FILING DATE: 11-SEP-1995
 ATTORNEY/AGENT INFORMATION:
  NAME: BAKER, Jean C.
  REGISTRATION NUMBER: 35,433
  REFERENCE/DOCKET NUMBER: 850586.90012
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (414) 277-5000
```

```
; TELEFAX: (414)277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2007 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Alignment Scores:
Pred. No.:
Score:                    0.0448        Length:            2007
Percent Similarity:      98.50          Matches:             60
Best Local Similarity:   33.10%         Conservative:        34
Query Match:             21.13%         Mismatches:         116
                          4.18%         Indels:              75
                              2         Gaps:                 8

US-09-807-459-2 (1-458) x US-08-743-637B-169 (1-2007)

Qy  163  TyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAla  182
              :::      ||| ||||  ::||||||  :::||||||::
Db  616  TACAAGATGATACCTTCGTTCCACTTTAAAACCGTTAAAAAAATGGATGAATTATTTAAGT  675

Qy  183  SerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAla  202
              |||    ::: |||||  ||||||
Db  676  GATTTCGCAAAAAAATTTCATCTTACAACT----------------------------  705

Qy  203  LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer  222
                                   :::    |||||::: ||| || :::
Db  706  --AATGAACAGAAAGTCGTAACTATCCTCTAGAAAAAGCCGACTTCACACTCATTAGGT  762

Qy  223  ArgLeuGlnHisIleThrSer------------------SerTyrLysAspTyrMetAsp  236
              ||| |||                              ||| ||| :::
Db  763  TATGTTGGTCCCATTAACCTCTGAGAGAATTAAAACAAAAAGAATATAAAGGCTTATAAGAT  822

Qy  237  -ThrGlnIleProAlaLeuProLysPheSerLeuMetValValGlnAr  256
              |||::: |||||  ||   ||| ||
Db  823  GATGCAGTTA-----------------TTGGTAAAAAGGGACTCG--------------  850

Qy  256  gLeuLeuAlaThrValAlaGlyTyrValAspThrProTrpTyrLysTrpTyrMetLy  276
              |||||| ||| ||  ||
Db  850  -------------------------------------------------------- 850

Qy  276  sLeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLysGl  296
                   |||||| :::      |||||||  :::||||
Db  851  ----AAAAACTTT----------------ACGATAAAAAGCTCCAACATGAA  882

Qy  296  uIleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuPh  316
                   ||||||:::|||||:::|||||::||||  :::|||||||||  :::||||||| ||
Db  883  GATGGCTATCGTGTCACAAATCGTTGAC-GATAATAGCAATAACAATCGACATACATTAAT  941

Qy  316  eGluAsnLysIleGlyGlnGlyThrValAlaGlyThrValAlaSpPhePheAsnLysGlnIleArgAspProse  336
                   |||||:::    ::::||     :::|||
Db  942  AGAGAAAAAG----------------------------AAAAAGAATGGCAAAGATATTCA  974

Qy  336  rLysAlaLeuLysGluLysValSerArgAsnAspAlaLysSerAspLeuPheGluAsnLysIleGl  356
                   |||||  ::: ||||||       ::|||||||   ||
Db  975  ACTAACTATTGATGCTAAAGTCAAAAGAGTATTTTATACAACATGAAAAATGATTATGG  1034

Qy  356  yGlnGlyThrValAspPheAsnAsnGluIleArgAspProSerLysAlaLeuLeuArg  376
                   |||:::|||  |||  |||||
Db  1035 CTCAGGTACTGCT-----------ATCCACCCTCAAACAGGTGAATTATTAGC  1076

Qy  376  gLysValSerThrGlyAlaGluProLeuPheGluAsnLysIleGlyGlnGlyThrValAls  396
                   ||||||||||||||||  ::: ||   ||
Db  1077 ACTTGTAAGCACACTTCATATGAGCTCATCCATTTATGTATGGCATGAGTGAACGGAAGA  1136

Qy  396  pPheIleAsnAsnGluIleArgAspProSerLysAlaLeuLeuIleArgLysValTyrThrGl  416
              ::: |||         :::     |||
Db  1137 ATAT---AATAAAATTAACCGAAGATAAAAAAGAACCTCTGCTCAACAAGTTCCAGATTAC  1193

Qy  416  uAlaAspAlaAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheAsnAsnLysGl  436
              ||| |||           ||:::|||||| |||
Db  416  GATTTCGCAAAAAAATTTCATCTTACAACT------------------  705
```

```
Db  1194 AACTTCACCAGGTTCAACTCAAAAAATTATTAACAGCAATGATGATTGGGTTAAATAAACAAAAC  1253
              |||||||             :::         |||||||
Qy  436  uIleArgAsp  439
              |||
Db  1254 ATTAGACGAT  1263

RESULT 27
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
;     APPLICANT: BERGERON, Michel G.
;     APPLICANT: OUELLETTE, Marc
;     APPLICANT: ROY, Paul H.
;     TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
;     TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
;     TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
;     TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
;     NUMBER OF SEQUENCES: 177
;     CORRESPONDENCE ADDRESS:
;     ADDRESSEE: QUARLES & BRADY
;     STREET: 411 East Wisconsin Avenue
;     CITY: Milwaukee
;     STATE: Wisconsin
;     COUNTRY: USA
;     ZIP: 53202-4497
;     COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/526,840B
;     FILING DATE: 11-SEP-1995
;     CLASSIFICATION: 435
;     PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/304,732
;     FILING DATE: 12-SEP-1994
;     ATTORNEY/AGENT INFORMATION:
;     NAME: BAKER, Jean C.
;     REGISTRATION NUMBER: 35,433
;     REFERENCE/DOCKET NUMBER: 850586.90012
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (414) 277-5000
;     TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2007 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Alignment Scores:
Pred. No.:
Score:                    0.0448        Length:            2007
Percent Similarity:      98.50          Matches:             60
Best Local Similarity:   33.10%         Conservative:        34
Query Match:             21.13%         Mismatches:         116
                          4.18%         Indels:              75
                              3         Gaps:                 8

US-09-807-459-2 (1-458) x US-08-526-840B-169 (1-2007)

Qy  163  TyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAla  182
              :::      ||| ||||  ::||||||  :::|||||||:
Db  616  TACAAGATGATACCTTCGTTCCACTTTAAAACCGTTAAAAAAAATGGATGAATTATTTAAGT  675

Qy  183  SerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAla  202
              |||    ::: |||||  ||||||
Db  616  GATTTCGCAAAAAAATTTCATCTTACAACT---------------------------  705
```

Alignment Scores:
Pred. No.:   0.0511   1829

```
RESULT 28
US-08-688-988-9
Sequence 9, Application US/08688988B
Patent No. 6096545

GENERAL INFORMATION:
; US-08-688-988-9
; APPLICANT: Lefebvre, Daniel D.
; APPLICANT: Malboobi, Mohammad A.
; TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
; FILE REFERENCE: PPL96-03
; CURRENT APPLICATION NUMBER: US/08/688,988B
; CURRENT FILING DATE: 1996-07-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 9
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana

US-09-807-459-2 (1-458) x US-08-688-988-9 (1-1829)

Score: 77                   Matches: 77
Percent Similarity: 97.50   Conservative: 76
Best Local Similarity: 35.09%   Mismatches: 132
Query Match: 17.66%         Indels: 151
DB: 4.13%                   Gaps: 21
                            Matches: 3
```

RESULT 29
PCT-US93-03077-2
Sequence 2, Application PC/TUS9303077
GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; APPLICANT: Gaynor, Richard B.
; APPLICANT: Wu, Foon Kin
; TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
; TITLE OF INVENTION: REGULATING GENE EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03077
; FILING DATE: 19930031
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,025
; FILING DATE: April 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: UTFD2270PCt
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1540
; TELEFAX: 713-749-2679
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3279 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
PCT-US93-03077-2

Alignment block 1

```
Qy   362 ------PheIleAsnAsnGluIleArgAspProSerLysAlaLeu---IleArgLys 377
              |||   :::                                          |||
Db  1303 GGATATGGAGAAGAACTAGGGCCTCAGATTCTGTTGCCTGGTGGTACCGGCTGATCATAAC 1362

Db  1363 AGGAAATATATATCTTCAGAGGCCATCTTTTTGAGTATGCCAAGAAGCTGTTTGCATCGACAAA 1422

Qy   378 Valser---ThrGlyAla------------GluAspLeu 385
              :::::   ||||||                  :::  |||
Db  1423 GTGAATGTTACAGAGATACTTTTGTATGTTCATTGTTGTTGGATAACTTCGAGTGGCAAGATGGT 1482

Qy   386 PheGluAsnLysIleGlyGlnGlyThrHrvalAspPheIleAsnAsnGluIleArgAspPro 405
              |||:::|||||||||||||                          |||    :::    |||
Db  1483 TACAAAAAACAGATTGGACTACTACGTTGATTTCAAAAAATAACCTTCACAGTT----- 1536

Qy   406 SerLysAlaLeuIleArgLysValTyrThrGlyAlaAspAspLeuPheGluAsnLysIle 425
              :::                                          ::::::
Db  1537 ------------TACGAGAAAGAATCC 1551

Qy   426 GlyGlnGlyThrHrvalAspPheIleAsnLysGlnIleArgAspProSer 441
              |||||:::|||:::|||:::||||||
Db  1552 GGCAAGTATTACAAGGATTTCCTCAGTCAAGGTGTTCGT---CCATCC 1596
```

Alignment block 2

Best Local Similarity: 20.20%
Query Match: 4.138
DB:

US-09-807-459-2 (1-458) x PCT-US93-03077-2 (1-3279)

Mismatches: 196
Indels: 130
Gaps: 19

```
Qy     9 AspValThrLysThrLeuLeuLeuAlaAlaSerGluSerVal------AspSerAlaAla 25
              :::|||||||:::||                          |||           |||
Db  1135 GAAGTAAAGTGAAACAATTAGTTATTATACCCACTGAGAGAACGAGAAATGGAAGAAAGTGGACCA 1194

Qy    26 AsnAlaTyrMetIleAsnSerArgAspMetSerAspTyrLeu---SerAlaValSerAspAsn 44
              :::|||                                                  :::
Db  1195 AGTGCAACTCCCTGTTAACTGTGAACAGCCTGATATCTTGGTTTTCTTCACACCAATAAAT 1254

Qy    45 PheGluGluArgGluCysSerGlnValProLysGlySerAsnHisSerTyrPhe 64
              :::||:::||                                          |||
Db  1255 GAAGGACAGACTGTGTAACAACAGCTG---GCTGACGCAGTTGACCCTGCTGAAAGT 1308

Qy    65 AlaTyrMetSerArgCysAlaLysGlnAsp---CysLeuThrLeuGlnSerLeuLysTyr 83
              :::|||                                 |||||:::          |||
Db  1309 CAGCCAGAAGCACTTTCTGAGAAGCAAGAAGATGTTTGCAAGACAGTTGAATTTCTGAATGAA 1368

Qy    84 ProLeuGluAlaLys---TyrGlnProLeuThrLeu---ProAspProTyrGlnLeuGlu 101
              |||:::          |||:::                                  |||||
Db  1369 AAGCTGGAAAAAAAGGGAGGGCTCAGTTATTATTATCTCTTAGTNAGGAAAAAAGCCACTTCTAGAA 1428

Qy   102 AlaAlaPheIleLeuPheLysGlu------------SerAspAlaAsnProAla 115
              |||                                        :::||||||
Db  1429 GAAGCTTTTGATAACCTGAAAGATGAAAATGTTCAGAGTGAAAGAGAAAAGCCAGTAGCATT 1488

Qy   116 AsnSerThrGluLysArgPheTrpMetArgPheArgGlyLysAsnHisSerTyrPhe 135
              :::|||                                             |||
Db  1489 TCTTCCTTGAAAGATGAGTTTTACTTCAAAGAATTGCAGAGACA------ 1530

Qy   136 HisAspLeuValPheAsnLeuLeuGlyLysAsnVal------ThrArgAsp 150
              |||                                       :::|||
Db  1531 ------GAAAAGAAAGTTCAACTAGCCTGCAAAGAGAGAT 1566

Qy   151 AlaAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyr 170
              |||:::||:::|||                                          |||
Db  1567 GCTCCTAAAAAAGAGAAATCAAAAACATAAAAGAAGAGAA------ 1602

Qy   171 TyrLysThrThrTyrThrAsnValAspGlyPheGlyAlaSerPhePheAsnLysLeuSerPhe 190
              |||                                                  :::|||
Db  1603 CTTGCACTAGATTAAAATAGTAGTGAAAACTGCAGACCTTTTGAAAGATGAGCAG 1662

Qy   191 ThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeuLeuGlnIleIleIleArgSerAsn 210
              |||||                                             ||||||
Db  1663 ATCCGAGGGGTTAATGGAGAGGAGAAAAACTTTCAAAACAGCAGCTGCACAAATTCTAAC 1722

Qy   211 Leu------ProLeuAspIleGlyThrGluHisSerValSerArgLeuGln 225
              |||      :::                                 :::|||
Db  1723 ATCATCAAGAAAATTAAGACGTAAAGACTAAAGAAGAGAATGAAAAATATGGTTGCAAAGCTGAAC 1782

Qy   226 HisIleThrSerSerTyrLysAspThrTyrMetAspThrGlnIleProAlaLeuProLysPhe 245
              :::|||                                             |||
Db  1783 AAAAAAGTTAAAGAGCTAGAAGAGAGTTG------ 1812

Qy   246 AlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrHrvalAlaGlyTyrVal 265
              |||                                                  :::|||
Db  1813 ------CAGCATTTGAAACAGGTGCTTGATGGC--- 1839

Qy   266 AspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgVal 285
              :::|||                                             |||
Db  1840 ------AAGAAGAGGTTGAGAAAAACAACATAGAGAAAAATATTAAAAAACTAAAT 1887

Qy   286 PheIleProThrLysLysPhePheAsnLysGluIleLeuArgGluProSerLysLysAlaLeuLys 305
              |||:::                                             :::|||
Db  1888 TCCATGGTTAGAGACGCCAAGAGAGAAAGATCTTGGCGTGTCTTCAGGTAGGACATGGATGAGAACTT 1947

Qy   306 GluLysValSerThrAspThrLysAspLeu 315
              |||
```

Alignment Scores:
Pred. No.: 0.134
Score: 97.50
Percent Similarity: 33.67%

Length: 3279
Matches: 99
Conservative: 66

Length: 3279
Score: 315

```
Qy    316  ---PheGluAsnLysIleGlyGlnGlyThrValAspPheAsnLysGluIleArgAsp  334
              ::|||||::|||          ||        |||
Db   1948  GAAGAAAAAGAACCGAAGTATTCAGGCTGCCCCTCGGATAGTGCATACAAGAACTTACTGAT  2007

Qy    335  ProSerLys------AlaLeuLysGluLysValSerAsnAspAlaLysAspLeuPheGlu  352
              |||          |||      |||
Db   2008  CTTCACAAAAGCCAAATGTCTGCAAAGGATAGTGAGGCACAGGAACCTGCTCTGACGGTGAA  2067

Qy    353  AsnLysIleGlyGln--------GlyThrValAspPheIleAsnAsnGluIleArgAsp  369
              |||    :::          |||        |||
Db   2068  ATGAAAAGCTAAAGAAGAACTTTCTGCAGCCATTAGAGAAGGCCCAAGAAGAAGCCCGTCAG  2127

Qy    370  ProSerLysAlaLeuIleLeuArgLysVal-----  378
              :::  |||
Db   2128  CAGCCAAGAAACATTAGCCATTCAAGTGGGGGACCTTAGGCTTGCATTGCCAGCGGTTACAGAA  2187

Qy    379  ------SerThrGlyAlaGluAspLeuPheGluAsnLysLysIleGlyGln  392
                    |||              :::
Db   2188  CAAGCGCGTGCCACAAAAGGAGGATTATTTACGCCATGACAAGAACTTCAGCAGAGA  2247

Qy    393  ---GlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysValAlaLeuIleArg  411
              |||        |||          :::  |||
Db   2248  CTCCAGGAGAAGCACAGAGAATCGAAACCAGAGAACTCGAGTCAAAGTGTTTCATCAACAACAGA  2307

Qy    412  LysValTyrThrGlyAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp  431
              :::  |||          |||          |||
Db   2308  CCAATTGCTTCGCACAAATAGAAAATTTGCA-AGCAAC-------CCTGGGATCCCAGAC  2357

Qy    432  PheIleAsnLysGluIleArgAspProSer  441
              |||||||||::::|||  |||
Db   2358  ATCGTCGTGGGAGAAATTAGAGAAGAAATCT  2387
```

RESULT 30
US-08-973-462-2

Sequence 2, Application US/0897346 2B
Patent No. 6191270

GENERAL INFORMATION:

APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 5361
TYPE: DNA
ORGANISM: P. falciparum
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(5361)
US-08-973-462-2

Alignment Scores:

```
Pred. No.:
Score:                      0.303          Length:          5361
Percent Similarity:        39.10%          Matches:           80
Best Local Similarity:     20.05%          Conservative:      76
Query Match:                4.13%          Mismatches:       138
                                           Indels:           105
                                           Gaps:              20
```

US-09-807-459-2 (1-458) x US-08-973-462-2 (1-5361)
DB:

```
Qy    109  GluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrpMetArgPheArgArg  128
              |||||:::|||                |||          |||
Db   2884  GAAAGTAATGAAAAATGTTCCAGAATTTAGAGAAGAA--------------------  2919

Qy    129  GlyLysAsnHisSerTyrPheHisAspLeuValPheAsn--LeuLeuGluGlyLys---Asn  146
              :::::                  |||||:::|||
Db   2920  --------------TTAAACGAAACTGTATTTAATACTGTATTAGATAAAAGTAGAG  2961

Qy    147  ValThrArgAspAlaAspLeuGluAsnPheAlaSerArgTyrLeuTyrMet  166
              :::                  :::
Db   2962  GAAACAGTAGAAAATTAGCCGGAGAAGAAGTTTAGAAAC--------------  2997

Qy    167  AlaThrLeuThrTyrTyrLysThrTyrThrAsnValAspGluPheGlyValAlaSerPheAsn  186
              :::                      :::
Db   2998  --------------------AATGAAATGGATAAAGGCATTTTTTAGT  3024

Qy    187  LysLeu------SerPheThrThrGlyLeuPheGlyTrp  197
              |||||||          |||::::|||
Db   3025  GAAATATTTGATAATGTAAAGGAATAACAAGAAAATTTATTAACAGGTATGTTT  3078

Qy    198  GlyIleLeuLysArgAlaLeuLysGlnIleIleLeuGluArgSerAsnLeuProLeuGlyThr  217
              |||                  :::
Db   3079  --------------CGAAGTATAGAAACCAGTATA-  3111

Qy    218  GluHisSerValSerArgLeuGlnHisIleIleThrSerSerTyrLysAspThrTyrMetAspThr  237
              |||          |||||||          :::
Db   3112  GAAGAAAAGGTTGATTGTAATGAAATGGGTTAGTCGATTTTGATTAATAATAGAAAAT  3171

Qy    238  GlnIleProAlaLeuProLysPheAlaLysSerArgPheSerLeu------  251
              :::
Db   3172  ATGAAAGAAAGGTTTATTAAAATAGAAAATATTCAAGTACTACTGAAGGTGTTCAAGGA  3231

Qy    252  MetValValGlnArgLeuLeuAlaThrValAlaLeuGlyTyrValAspThrProTrpTyrLys  271
              |||||||          |||          |||
Db   3232  ACTGTAACTGAACACTGTAGAACAAAAATGTATATGTGGATGTTGATCTGCTATGAAA  3291

Qy    272  LysTrpTyrMetLysLeuLysAsnPheMet------ValAsnArgValPheIleProThr  289
              ::::::                  :::  :::|||
Db   3292  GATCAATTTTTAGGAATATTAAATGAGGCAGGAGGGTTGAAAGAAAATGTTTTTAATTTG  3351

Qy    290  LysLysPhePheAsnLysGlu------IleArgGlu-----ProSerLysAla  303
              :::                  |||          |||
Db   3352  GAAGATGTATTTAAAAGTGAAGTTGATGAAGAAAATTACTGTGAGAAGAAATTAAGGATGAACCG  3411

Qy    304  LeuLysGluLysValSerThrAspPheLysAspLeuPheGluAsnLysLysIleGlyGlnGly  323
              |||||||:::|||          |||          :::
Db   3412  GTTCAAAAAAGAGGTAGAAAAAGAAACGAAACCTGTTAGTATATTA---GAAATGGAAGAAAAT  3468

Qy    324  ThrValAspPhePheAsnLysGluIleArgAspProSer-----LysAlaLeu  339
              |||          |||          :::
Db   3469  ATTGTAGATGTATTTAGAGGAGAAAAAGAGATTTAAGCAGACAAGATATGAGTA  3528

Qy    340  LysSerGlu------LysValSerAsnAspAlaLysAspLeuPheGluAsn---LysIleGly  356
              :::|||              :::  |||
Db   3529  GAAGAACTCCATAGAAAATATCCTTCAGATTCTAAAGAAGAAAACTGAATCTATTAAAGATAAA  3588

Qy    357  GlnGlyThrValAspPheIleAsnAsnGluIleArg------AspProSerLys  372
              |||          |||          :::  |||
Db   3589  GAAAAAGATGTTTCACTGAGTTCGTTGAAGACAATGATATGGAAGTGTT  3648

Qy    373  AlaLeuIleLeuArgLysValSerThrGlyAlaGluAspLeuPheGluAsnLysLysIleGlyGln  392
              |||          :::  |||          |||
Db   3649  GAGAAAGTTTTAGAATTGAAAAATATCGAAGAGGAGTTAATCGAAGATGCGTT--  3702

Qy    393  GlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleLeuArgLys  412
              |||          |||          :::
Db   3703  --------------GAAATAAATGACAATTACTAGCAAACTTATTGAAGAA  3738

Qy    413  ValTyr------ThrGluAlaAsp---  425
              :::                  |||||::::|||
Db   3739  ACTCAAGAGTTAAATGAAGTAGAAGCAGATTTAATAAAATAAAAGATATTGGAAAAAATTAAAAGA  3798

Qy    426  GlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIle  445
              :::  |||::||||||||||
Db   3799  TTAGAAAAAGCATTATCAGAGAATTCTAAAGAAAATAATAAGATGATTACATTA  3858

Qy    446  ArgLysVal------SerThrGluAlaAspAsnLeuLeuGlu  457
```

```
Db  3859 GAAAAGTTATTGAAGAGAGAACAATGATATAACGACGACGTTGGAATGAAGAAGTTGTAGAA 3915
          |||||||                  |::::||||          |||  :::||||
Qy       GAAAAGTTATTGAAGAGAGAACAATGATATAACGACGACGTTGGAATGAAGAAGTTGTAGAA

RESULT 31
US-08-973-462-1
; Sequence 1, Application US/0897346 2B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: P. falciparum
DB:

US-09-807-459-2 (1-458) x US-08-973-462-1 (1-6152)

Alignment Scores:
Pred. No.:
Score:              0.381
Percent Similarity: 97.50
Percent Identity:   39.10%
Best Local Similarity: 20.05%
Query Match:        4.13%
```

Length:	6152
Matches:	80
Conservative:	76
Mismatches:	138
Indels:	105
Gaps:	20

```
Db  3164 ----------------TTAAACGAAACTGTATTTAATACTGTATTAGATAAAAGTAGAG 3205
                          :::::||||  :||||||||||||||||||  ||||
Qy   129 GlyLysAsnHisSerTyrPheHisAspLeuValPheAsn---LeuLeuGluLys---Asn 146
         ||||||||||                    ::||||||||  :::||||||||||||||
Db  3242 -----------------AATGAAAATGGAATAAAAGCATTTTTTAGT 3268
Qy   167 AlaThrHisLeuTyrPheLysThrTyrThrAsnValAspGluPheGlyAlaSerPhePheAsn 186
         :::|||                   |||||||||||||  ::::||||
Db  3206 GAAACAGTAGAAAATTAGCGGAGAAAGTTTAGAAAAC----------------------- 3241
Qy   109 GluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrpMetArgPheArgArg 128
         |||||||:||      ||||||      ||||          |||  ||||||
Db  3128 GAAAGTAATCAAAAAATGTTGCAGAGAATTTAGAGAAA---------------------- 3163
Qy   147 ValThrArgArgAspAlaThrAspIleGluAsnPheAlaSerArgArgTyrLeuTyrMet 166
         :::||::::||||||                       |||||||
Db  3205 -----------------TTAAACGAAACTGTATTTAATACTGTATTAGATAAAAGTAGAG 3205
Qy   187 LysLeu---------- -----SerPheThrThrGlyLeuPheGlyTrp 197
         :::::                    ||||||:||||||||
Db  3322 GAAATATTTGATATAAATGTAAAAGGAATACAAGAAAAATTTATTAACAGGTATGTTT----- 3269
Qy   198 GlyIleLysArgAlaLeuLysGlnIleIleIleArgSerAsnLeuProLeuAspIleGlyThr 217
         |||:::::::|||:::::::|||                 |||  :::
Db  3355 ------------CGAAGTATAGAAACCAGTATA----------------GTAATCCAATCA 3323
Qy   218 GluHisSerValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThr 237
         ||:||                                      ||:
Db  3415 GAAGAAAAGTTGATTTGAATGAAAATGGTTACTTCGATTTTAGATAATATAGAAAAT 3356
Qy   238 GlnIleProAlaLeuProLysPheAlaLysArgPheSerLeu---------------- 251
         ::::||                       |||
Db  3475 ATGAAAGAAGGTTTATTAAATAAATTTCAAGTACTACGAAGGTGTTCAAGAA 3416
Qy   252 MetValValGlnArgLeuLeuAlaThrArgValAlaGlyTyrValAspThrProTyrLys 271
         |||  :::                   ||| ::: |||  |||  |||
Db  3535 ACTGTAACTGAACAAATGTATATATGTGGATTGTGATGTTCCTGCTATGAAA 3476
Qy   272 LysTrpTyrMetLysLeuLysAsnPheMet------ValAsnArgValPheIleProThr 289
```

```
Db  3595 GATCAATTTTAGGAATATTAAATGAGGCAGGAGGGTTGAAAGAAAATGTTTTTTAATTG 3536
          ||                    :::                    :::|||
Qy   290 LysLysPhePheAsnLysGlu--------------IleArgGlu----ProSerLysAla 303
         |||                       ::::|||                  |||:::
Db  3655 GAAGATGTATTTAAAAGTGAAAGTGATGTAATTACTGTAGAAGAAAATTAAGGATGAACCG 3596
Qy   304 LeuLysGluLysValSerThrAspPheLysAspLeuPheGluAsnLysIleGlyGlyGly 323
         :::::|||:::|||                              ::::|||
Db  3712 GTTCAAAAAAGAGGTAGAAAAAGAAAAAACTGTTAGTATTATTGAA----GAAATGAAAAAAT 3656
Qy   324 ThrValAspPhePheAsnLysGluIleArgAspProSer-----------LysAlaLeu 339
         :::|||                  :::|||           |||||
Db  3772 ATTGTAGATGTATTAGAGGAAGAAAGAGAAGATTTAACGACAAGAGATGATGCAGTA 3713
Qy   340 LysGlu------LysValSerAsnAspSerAlaLysAspLeuPheGluAsn---LysIleGly 356
         |||                      ||||||:::|||||::: :::|||
Db  3832 GAAGAATCCATACAAAATATCTTCAGATTTCTCAAGAAGAAGAAACTCATTAAAGATAAA 3773
Qy   357 GlnGlyThrValAspPhePheAsnLysGluIleArgAspProSer----------AspProSerLys 372
         ::::||                         |||  :::|||          |||
Db  3892 GAAAAAGAAGTTTCACTAGTTGTTGGAAGAAGTTCAAGACAATAGATGTGAAAAAGTGTT 3833
Qy   373 AlaLeuIleArgLysValSerThrGlyAlaGluLeuAspLeuPheGluPheGluGln 392
         :::                        :::|||      :::|||:::::
Db  3946 GAGAAAGTTTTAGAATTGAAAAAATATGGAAGAGGAGTTAATGAAGAAGATGCTGTT----- 3893
Qy   393 GlyThrValAspPheIleAsnAsnGluIleLeuArgAspProSerLysAlaLeuIleArgLys 412
         |||                       :::|||||||||||                |||
Db  4042 GAAATAAATGACATTACTAGCAACAAACTCATTAAAGATAAA 3947
Qy   413 ValTyr----------------ThrGluAlaAsp------AspLeuPheGluAsnLysIle 425
         ||||||                  ::::||||||
Db  4102 TTAGAAAAAGCATTATCAGAAGAAGATTCTAAAGAAAGAAATAATAGATCCAAAAGATAGATACATTA 4043
Qy   426 GlyIleGlnGlyThrValAspPheIleAsnAsnGluIleLeuArgAspProSerLysAlaLeuIle 445
         |||                          :::|||           |||
Db  4159 GAAAAAGTTATTGAAGAGAGAACAATGATATAACCGACGACGTTGGATGAAGTTGTAGAA 4103
Qy   446 ArgLysVal-----------------SerThrGluAlaAspAsnLysLeuLeuGlu 457
```

```
RESULT 32
US-08-799-138-5
; Sequence 5, Application US/08799138
; Patent No. 5994053
; GENERAL INFORMATION:
; APPLICANT: Verma, Desh Pal
; TITLE OF INVENTION: PHRAGMOPLASTIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CALFEE, HALTER & GRISWOLD
; STREET: 800 SUPERIOR AVENUE
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,138
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLRICK, MARY E
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
```

; TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2211 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 175..2004
US-08-799-138-5
DB:

Alignment Scores:
Pred. No.:
Score: 0.0807
Percent Similarity: 97.00
Best Local Similarity: 35.90%
Query Match: 17.95%
                           4.11%
DB: 2

Length: 2211
Matches: 63
Conservative: 63
Mismatches: 125
Indels: 100
Gaps: 16

US-09-807-459-2 (1-458) x US-08-799-138-5 (1-2211)

```
Qy  139  ValPheAsnLeuLeuGlyLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsn 158
         |||:||| ||||||||||:::::||||||||||||:::|||||||||||::||||||
Db  892  GTTGTGAATAGATCACAACAAGACATAAACAACAGTTGACAATGAGTTGCTGCTAGGCGT 951

Qy  159  PheAlaSerArgThrLeuThrTyrThrTyrThrArgAsnValAsp 178
         |||:|| ||||||||:||||||||||| |||
Db  952  AGAGAACGTGAGTAC--TTTAATAGTACCCCTGAATATAAACACCTTGCAAAC---- 1002

Qy  179  GluPheGlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly 198
         |||: |||
Db  1003 AGAATGGGTTCTGAACATCTGGCGAAGATG 1032

Qy  219  HisSerValSerArg------ 223
         :||::: ||
Db  1033 CTCTCAAAGCATTTGGAGACAGTAATCAAGTCCAAAAATTCCT------GGCATTCAA 1083

Qy  199  IleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlu 218
         ||||::|||:||:||||||::::||
Db  1084 TCCCTAATTAACAAACAAATTGCCGAACTTGAAGCTCAACTAACTCGTTTAGGAAAACCT 1143

Qy  224  ------LeuGlnHisIleThrSerSer------ 230
         ::: |||
Db  1144 GTTGCAGCTGATCCTGGGGAAAGTTGTATGCCTATCATGGAAATATGCCGCTCATTTGAT 1203

Qy  231  ------TyrLysAspThrMet-- 235
         :||:|||:::
Db  1204 CAAATATTTAAAGACCATCTTGATGGCGTGCGGCCCTGGAGGTGATAAAAATTTATAATGTC 1263

Qy  236  --AspThrGlnIleProAlaLeuProLys-- 251
         ||| |||:|||:: PheAlaLysArgPheSerLeu
Db  1264 TTTGACAATCACCTCCCTGCTCGTTTAAAAAGGTTGCAGTTGATAAGCCAGCTTTCAAATG 1323

Qy  252  MetValValGlnArgLeuLeuAlaThrValAlaLeuGlyTyr------ ValAspThrPro 268
         ||||||
Db  1324 GAAAAATAAGGAAACCTTATTACAGAGCCTCATCTAATAGCTCCA 1383

Qy  269  TrpTyrTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgValPheIlePro 288
         |||
Db  1384 ------GAACAAGGATACCGTCGCCTAATTGAATCTTCTAATAACTATTAGGGCCCT 1437

Qy  289  ThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysVal 308
         ||| ||| ||||||
Db  1438 GCTGAGTCAGCTGTTGAT---GCGGTTCACTCCCTGTTAAAGGACTTGGTTCACAAAGCT 1494

Qy  309  SerThrArgAspThrLysAspLeu------ PheGluAsnLysIleGlyIleGly 323
         :::|||:::||| |||:::::|||||
Db  1495 ATGAGTGAGACTTTGGACTTGAAGCAGTATCCTGGTCTCCGGGTTGAGGTTGGGCTCCA 1554

Qy  324  ThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysVal 343
         :: ::||||||||
Db  1495 ATGAGTGAGACTTTGGACTTGAAGCAGTATCCTGGTCTCCGGGTTGAGGTTGGGCTCCA 1554
```

RESULT 33
US-09-392-362-5
Sequence 5, Application US/09392362
Patent No. 6248868
; GENERAL INFORMATION:
;   APPLICANT: Verma, Desh Pal
;   TITLE OF INVENTION: PHRAGMOPLASTIN
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CALFEE, HALTER & GRISWOLD
;   STREET: 800 SUPERIOR AVENUE
;   CITY: CLEVELAND
;   STATE: OHIO
;   COUNTRY: USA
;   ZIP: 44114
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/392,362
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/799,138
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: GOLRICK, MARY E
;   REGISTRATION NUMBER: 34,829
;   REFERENCE/DOCKET NUMBER: 22727/00139
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (216) 622-8458
;   TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2211 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 175..2004
US-09-392-362-5

```
Db  1555 TCTGTTGATTCACTCGAAAGA--...ATGAGGGATGAAAGCAAA-------------- 1593

Qy  344  SerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIle 363
         ||| ::: LeuIleArgLysValSerThrGly
Db  1594 ---AGAGCAAACACTCCAGCTAGTTGATATCGGAGTGTGGCTATCTGCACTGGTTGATTCTTTT 1650

Qy  364  AsnAsnGluIleArgAspProSerLysAlaLeu------ LeuIleArgLysValSerThrGly 381
         :::||| :::
Db  1651 CGGAAGCTTCCTCAAGATGTTGATAAGGGTGGGCAATCCCACACATTCAAATTGTGATAGA 1710

Qy  382  AlaGluAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAlaAsn--- 400
         ::|||||| :::||| :::|||
Db  1711 TATAATGATTCATATCTAAGGCAGAAGTTGGAACCACAAATTTGTCGATATAGTCAATATGGTC 1770

Qy  401  ------ GluIleArgAspPro 405
         |||||:::|||
Db  1771 TGTCCTACTCTGCGGCATTCAAATTCCCAAGCTCCATCGTCTATTGTCAAGTGCGGGAGGCA 1830

Qy  406  SerIleAlaLeuIleArgLysValThrTyrThrGlu 416
         :::||||||
Db  1831 AAACGAAGTCTACTTGATCACTTTTTTTACGGAG 1863
```

Alignment Scores:
Pred. No.:
Score: 0.0807
Percent Similarity: 97.00
Best Local Similarity: 35.90%
                           17.95%

Length: 2211
Matches: 63
Conservative: 63
Mismatches: 125

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Query Match:    4.118     Indels:  100
DB:             4         Gaps:    16

US-09-807-459-2 (1-458) x US-09-392-362-5 (1-2211)

Qy  139 ValPheAsnLeuLeuGluLysAsnValThrArgAspAlaAspIleGluAsn                158
Db  892 GTTGTGAATAGATACACAACAAGACATAAAACAAGAAGATTGACATGATTGCTCTAGGCGT      951

Qy  159 PheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAsp        178
Db  952 AGAGAACGTGAGTAC---TTTAATAGTACCCCTGAATATAAAACACCTTGCAAAC------      1002

Qy  179 GluPheGlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly        198
Db 1003 AGAATGGGTTCTGAACATCTGGGCAAGATG------                              1032

Qy  199 IleLysArgAlaLeuLysGlnIleIleIleGluArgSerAsnLeuProLeuAspIleGlyThrGlu  218
Db 1033 CTCTCAAAGCAATTGGAGACAGTAATCAAGTCCAAAATTCCT------GGCATTCAA        1083

Qy  219 HisSerValSerArg---------                                           223
Db 1084 TCCCTAATTAACAAAAACAATTGCCGAAACTTGAACTAACTCGTTTAGGAAAACCT         1143

Qy  224 ------LeuGlnHisIleThrSerSer------                                  230
Db 1144 GTTGCAGCTGATGCTGGGGAAAGTTGTATGCTATCATGGAAATATGCCGCTCATTTGAT      1203

Qy  231 -----TyrLeuSerAspTyrMet------                                      235
Db 1204 CAAATATATTAAAGACCATCTTGATGGCGTGCGGCCTGGAGGTGATAAAATTATAATGTC      1263

Qy  236 ---AspThrGlnIleProAlaLeuProLys------PheAlaLysArgPheSerLeu          251
Db 1264 TTTGACAATCAGCTCCCTGCTTTTAAAAGGTTGCAGTTTGATAAGCAGCTTTCAATG        1323

Qy  252 MetValValGlnAsnArgLeuLeuAlaThrValAlaLaGlyTyr------ValAspThrPro     268
Db 1324 GAAAATATAAGGAAAACTTATTACAGAAGCTGATGGGTACCAGCCTCATCTAAATAGCTCCA    1383

Qy  269 TrpTyrTyrLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgValPheIlePro       288
Db 1384 -----GAACAAGGATACCGTCGCCTAATTGAATCTTCTAATAACTATTAGGGGCCCT         1437

Qy  289 ThrLysLysPhePheAsnLysGluIleLysGluProSerLysAlaLeuLysGluLysLysVal    308
Db 1438 GCTGAGTCAGCTGTTGAT---GCGGTTCACTCCCTGTTAAAGGACTTGGTTCACAAAGCT      1494

Qy  309 SerThrAspThrHisLysAspLeu------                                     323
Db 1495 ATGAGTGAGACTTTGGACTTGAAGCAGTATCCTGTCTCCGGGTTGGGGCTGCA            1554

Qy  324 ThrValAspPhePheAsnLysGluIleGluArgAspProSerLysAlaLeuLysGluLysVal    343
Db 1555 TCTGTTGATTCACTCGAAAGA---ATGAGGGATGAAAGCAAA------                  1593

Qy  344 SerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle       363
Db 1594 --AGAGCAACAACTGCAGCTGTAGTTGATATGGAGTGTGGCTACTGACTGTTGATTTCTTT     1650

Qy  364 AsnAsnGluIleArgAspProSerLysAla------LeuIleArgLysValSerThrGly       381
Db 1651 CGGAAGCTTCCTCAAGATGTTGATAAGGGTGGCAATCCCACACATTCAATTTGTGATAGA      1710

Qy  382 AlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsn---       400
Db 1711 TATAATGATTCATATCTTAAGGCGAATTGGAACCACAATTTGTCATATGTCAATATGGTC      1770

Qy  401 ----------GluIleArgAspPro                                          405
Db 1771 TGTGCTACTCTGCGGCATTCAATTCCCAAGTCCATGTCTGTTCATTGTCAAGTCGCGGGAGGCA  1830
```

```
Qy  406 SerLysAlaLeuIleArgLysValThrTyrThrGlu                              416
Db 1831 AAACGAAGTCTACTTGATCACTTTTTTACCGAG                                1863
```

```
;  TITLE:
;  JOURNAL:
;  VOLUME:
;  ISSUE:
;  PAGES:
;  DATE:
;  DOCUMENT NUMBER:
;  FILING DATE:
;  PUBLICATION DATE:
;  RELEVANT RESIDUES IN SEQ ID NO:
US-08-094-889-2

Alignment Scores:
Pred. No.:              0.143
Score:                 97.00
Percent Similarity:    33.21%
Percent Identity:      18.70%
Best Local Similarity: 4.11%
Query Match:              1

                       Length:        3123
                       Matches:         98
                       Conservative:    76
                       Mismatches:     184
                       Indels:         166
                       Gaps:            21

US-09-807-459-2 (1-458) x US-08-094-889-2 (1-3123)

Qy   13 ThrLeuLeuAlaAlaSerGluSerValAspSerAlaAlaAsnAlaThrMetIleAsnSer 32
           |||::||        ::||||     :|||||
Db  488 ACGATGGTAGAGCCTGAGTCGACTGAAAACGGCCGTGTTGCGGCAGGCACTGCAGGGACCTG 547

Qy   33 AspMetSerAspThrTyrLeuSerAlaValAlaSerAsp---AsnPheAlaGluArgIleCysSer 51
           ||||||||||:||        ||:||||        :::|||
Db  548 GATATGGCGGACGCTCATGTACGGCTTCTTTCACATCTGAAAATTGTAGAGGAGCACTAGAA 607

Qy   52 GlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSerArgCysAla 71
           |||                        :::    :::
Db  608 GCAGTGAAAAAATGCAACAAAATGAACACAGATTTAGCAAAATCGGTTC 652

Qy   72 LysGlnAspCysLeuThrLeuGlnSerLeuLysThrTyrProLeuGluAlaLysTyrGlnPro 91
           |||||||:|        |||    |||    :::|||
Db  653 AAAGAAATTTGGAAAGAGATGGTGAAACTGAATTATGTAGCTCCACGGCCAGACAG--- 709

Qy   92 LeuThrLeuProGlnAspPro--- 97
           ||||||
Db  710 ---GAGCTGAAAAGATCCTCCACTCCAGGGATGAAAATGGCTGCAGCTCGAGGTGCTCTGAAG 766

Qy  132 HisSerTyrPheHisAspLeuValPheAsnLeuLeuGlyLys------------ 145
           ||||||:||||||:||
Db  842 ----AGAGACTATATGTCTTCAAGCAAGTTCAAGAAAGCAAATTGCTGGTATTTCC 889

Qy  146 AsnValThrArgAspAlaAspAlaThrArgGluAsnPheAlaSerArgTyrLeuTyr 165
           ||||||    :::
Db  890 AACGCTGCCCAGCCACCTCACCCACCTGAT---GAAAAC--- 925

Qy  166 MetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
           |||        |||    |||    :::
Db  926 ----AAGGGGCATACTGGCATTGGAGACGTTGCCTGCGACACTAAAT 967

Qy  184 --PhePheAsnLys--- 197
           :::||||:||::||
Db  968 GAATTTGATAACAAAATCATCTTAGACCCCATGACGTTCAGCGAGGCCCCGCCTTCAGGCCC 1027

Qy  198 GlyIleLysArgAlaLeuLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThr 217
           ||:||:        |||||||
Db 1028 TCTCTGAGGAGGAGGCTGGAGCAGCATTATC------------ 1057

Qy  218 GluHisSerValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThr 237
           |||    |||        ::||
Db 1058 -----AGTGGGGCAGCGCCTGATGGCAGAGACTCCTCCCACGCGGGGATGACCGGAGGAAG 1111

Qy  238 GlnIleProAlaLeuProLysPheAlaLysPheSerLeuMetValValGlnArgLeu 257
           ::||||        |||        ---
Db 1112 CGCATCGTAGCTGAGTGCAGAAACGGCGTGTTGCGGCAGGCACTGCAGGGACCTG------- 1162

Qy  258 LeuAlaThrValAlaLaGlyTyrValAspThrProTrpTyrLysLysTrpTyrMetLysLeu 277
                                                        |||
Db 1163 ------------------------------------------------CTC 1165

Qy  278 LysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLysGluIle 297
           ||||||        |||    |||
Db 1166 AGGCAGTACATGAACAAATACT---GGAAGGAAAGAGAAG 1201

Qy  298 ArgGluProSerLysAlaLeuLysGluLysValSerThrArgThrLysAspLeuPheGlu 317
           |||||||||||::||        :::||||
Db 1202 GGGGAGCCCACTCAACATTGCTATTGACACAGATGACCAAGAAAACACGAGAGACCTT---CGA 1258

Qy  318 AsnLysIleGlyIleGlyThrValAspProPheAsn----------- 329
           :::|||
Db 1259 AGACAACTCCCGAAGGCCAGTAAATGGATCATATATCAGATTCGTTCCTGGGGAGACCAATGTG 1318

Qy  330 ------------------------------------------ 330
           |||||||:::::||||:::
Db 1319 CCAATTGCTGGTTCTCATCGAGGCTCCCAAAAGGGTTAATGAGAAGAAGTGAAGGAGTAC 1378

Qy  336 SerLysAlaLeuLysGlu--- 349
           :::||||
Db 1379 ----LysValSerAsnAspAlaLysAsp----LysSerAsnAspAlaLysAsp 1438

Qy  350 LeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsnAsnGluIleArgAsp 369
           :::        |||    |||        :::|||
Db 1439 ATCTCAAATAATGAAGAAGAAGGTGTGAAGCTAGTGCGGTATGGCGAGCAACACAGATTGATAGT 1498

Qy  370 ProSerLysAlaLeuLeuGluArgLysValSerThrArgThrLysAspLeuPheGluAsnLys 389
           :::||||        |||:::
Db 1499 CTGTGCCCCCAGGTAATAAATGCTGCGCGGATGATTCCCTCGTTTCAGAAAAATCAT 1555

Qy  390 IleGlyIleGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeu 409
           |||    |||        :::
Db 1556 GTAGCACAGGACAACATGGATGTCTTTAAGGATCAGTGGGAGAAACAAGTGCGAGTTCTC 1615

Qy  410 IleArgLysVal-------TyrThrGluAlaAspAspLeuPhe---------GluAsnLys 424
           |||        |||    |||
Db 1616 ACTGAAGCAGTTGATGACATCACTTCAGTGGATGATTTCCTCGTTTCAGAAAAATCAT 1675

Qy  425 Ile--------------GlyIleGlyThrValAspPheIle 433
           |||        :::
Db 1676 ATTCTGGAAACAGTGAACAAAATGTGATTGCCTTCTCCAAGAGGGAGATGTCGATACCCTG 1735

Qy  434 AsnLys--------GluIleArgAspProSerLysAlaLeuIleArgLysValSerThr 450
           ||||||        :::
Db 1736 GATAGAACTGCTGGGGGCCCCATCCGAGGCCGTGCCAGCCAGAGTCATTCACATCATTAATGCA 1795

Qy  451 GluAlaAspAsn 454
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Db 1796 GAGATGGAAAAC 1807
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;  COUNTRY: USA
;  ZIP: 19406-2799
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: Patentin Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: PCT/US94/01149
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 149,150
;  FILING DATE: 05-NOV-1993
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 013,415
;  FILING DATE: 01-FEB-1993
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 108,914
;  FILING DATE: 18-AUG-1993
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 751,896
;  FILING DATE: 30-AUG-1991
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 837,773
;  FILING DATE: 18-FEB-1992
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 387,200
;  FILING DATE: 28-JUL-1989
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 238,801
;  FILING DATE: 02-NOV-1988
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 645,732
;  FILING DATE: 30-AUG-1984
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Baumeister, Kirk
;  REGISTRATION NUMBER: 33,833
;  REFERENCE/DOCKET NUMBER: P50134 PCT
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 215-270-5096
;  TELEFAX: 215-270-5090
;  INFORMATION FOR SEQ ID NO: 31:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 912 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: double
;  TOPOLOGY: unknown
;  MOLECULE TYPE: DNA (genomic)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: 1..912
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PCT-US94-01149-31

US-09-807-459-2 (1-458) x PCT-US94-01149-31 (1-912)

Alignment Scores:
Pred. No.:
Score:                   0.0214
Percent Similarity:      96.50
Best Local Similarity:   34.15%
Query Match:             20.91%
DB:                      4.09%
                         5
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                                                Length:          912
                                                Matches:         60
                                                Conservative:    38
                                                Mismatches:      84
                                                Indels:          105
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Qy    209 SerAsnLeuProLeuAspIleGlyThr------------------------GluHisSerValSerArg 223
Db     82 GGTGATGCGCCCATTCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGGAGGAGGGGC 141
Qy    204 ------------------------------------------------LysGlnIleIleArg------ 208
Db     22 AGCTTTCAGGTAGATTGCTTTCTTTGGCAATGTCCGCAAACGAGTTGCAGACCAAGAACTA 81
Qy    189 SerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeu------------------ 203
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Db    142 AGCACTGTCTTGGTCTTCTGGACATGCAGAGACCCACACGTGCTGGAAAGCAGAGTAGTGGACGCG 201
Db    202 ATTCTGAAAGAAGAAGAATCCGATGAGGCACTTAAAATGACCAATCCCAGACCCCGGT------- 255
Qy    244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaAlaGly 263
Qy    256 ------------------------------------------------CTATTTGGAGGCATTGCCGGT 276
Db    264 TyrValAspThrProTrp----------TyrLysLysTrpTyr------------ 274
Db    277 TTTATTGAAGGGGGATCGACTGGAAATGATAGATGGGTATCATCAAGAAT 336
Qy    275 ------------------------------------------------MetLysLeuLysAsnPheMet 281
Qy    337 GAACAGGGATCAGGCTATGCACCGGATCAAAAAGCACACAAAAATGCCATTAACGGGATT 396
Db    282 ValAsnArgVal------------------------------PheIleProThrLysLys 291
Db    397 ACAAACAAGGTGAACTCTGTTATCGGAGAAAATGACATTCAATTCACAGCTGTGGGTAAA 456
Qy    292 PhePheAsnLysGluIleArgGluProSerLysValSerAlaLeuLysGluLysValSerThrAsp 311
Qy    457 GAATTCAACAAA--TTAGAAAAAGGATGGAAAAATTTTAAATAAAGAAGTTGATGATGGA 513
Db    312 ThrLysAsp-------------------------LeuPheGluAsnLysIleGly 321
Db    514 TTTCTGGACATTTGGACATAATAATGCAGAATTGTTTAGTTCTACTGGAAAAT------- 564
Qy    322 GlnGlyThrValAspPhePheAsnLysGluIleIleArgAspProSerLysValSerAlaLeuLysGlu 341
Qy    565 GAAAGGACTCTGGATTCCATGACTCAAAATGTGAAGAATCTGTATGAGAAAGTAAAAGC 624
Db    342 LysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlyThrValAsp 361
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Qy    362 Phe------IleAsnAsnGluIleArgAspProSerLysValSerAlaLeuLeuIleLeuArgLysVal 378
Qy    670 TTCTACCACAAGTGTGACAATGAA--------------TGCATGGAAAGTGTA 708
Db    379 SerThrGlyValaGluAspLeu------PheGluAsnLysIleGlyThr 394
Db    709 AGAAATGGGACTTATGATTATCCCAAATATTCAGAAGAGTCAAAGTTGAACAGGGAAAG 768
Qy    395 ValAspPheIleAsnAsnGlu 401
Qy    769 GTAGATGGAGTGAAAATTGGAA 789
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Qy    209 ...
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US-08-471-033-31
; Sequence 31, Application US/0847103311
; GENERAL INFORMATION:
; Patent No. 5770696
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
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ZIP: 10532
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/471,033
  FILING DATE:
PRIOR APPLICATION DATA:
  CLASSIFICATION: 530
  APPLICATION NUMBER: US 08/314,594
  FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/218,018
  FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/037,057
  FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Pace, Gary M.
  REGISTRATION NUMBER: P-40,403
  REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SQLv3
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 919-541-8689
  TELEFAX: 919-541-8582
INFORMATION FOR SEQ ID NO: 31:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2612 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  HYPOTHETICAL: NO
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 118..2484
  OTHER INFORMATION:
  OTHER INFORMATION: /note= "Native DNA sequence
    encoding VIP3A(b) from AB424"
US-08-471-033-31

Alignment Scores:
Pred. No.:
Score: 0.123
Score: 96.50
Percent Similarity: 36.18%
Best Local Similarity: 20.28%
Query Match: 4.09%
DB: 1

Length: 2612
Matches: 102
Conservative: 80
Mismatches: 202
Indels: 119
Gaps: 24

US-09-807-459-2 (1-458) x US-08-471-033-31 (1-2612)

Qy   4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
         ::||||| ::: ||||| :::|| :||||::::||
Db   235 ACGGATACAGGTGGTGATCTACC----------------------CTAGACGAA 267

Qy   24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
         |||||||||| ||| ::::||||||
Db   268 ATTTTAAGAGAATCAGCACTACTAAAATGATATTTCTGGTAAAATGGAAGGGGTGAAATGGA 327

Qy   44 AsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
               ||| ||| ::::
Db   328 AGCTTAAATGATCTTATCGCACAG----------------GGAAACTTAAATACAGAATTA 372

Qy   64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
         ::: ||||| ||| ::: |||
Db   373 TCTTAAGGAAAATATTAAAATTCCAAATGAACAAAATCAAGTTTTAAAATGAGTTAATAAC 432

Qy   84 ProLeuGluAla----------------------------------LysTyrGlnPro 91
         ||| |||
Db   433 AAACTCGATGCCATAAAATACGAATGCTTCGGGTATATCTACCTAAAATTACCTCTATGTTG 492

Qy   92 --LeuThrLeuProAspProTyr----------Gln 99
                                                              |||:::||| |||
Db   493 AGTGATGTAATGAAACAAAATTATGCGCTAAGTCTGCAAATAGAATACTTAAGTAAACAA 552

Db   493 AGTGATGTAATGAAACAAAATTATGCGCTAAGTCTGCAAATAGAATACTTAAGTAAACAA 552

Qy 100 LeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnPro---AlaAsnSerThr 118
         |||::: |||||||||| :::|||
Db   553 TTGCAAGAGATTTCTGATAAGGTTGGATATTATTAATGTAAGTGTACTTAAGTACCTTACA 612

Qy 119 GluLysArgPheTrpMetArgPheArgGlyLysAsn---HisSerTyrPheHisAsp 137
         :::::::|| :::
Db   613 CTTACTGAAATTACACCTCCGTATCAAAAGGATTAAATATGTGACCAGAAAAATTTGAGGAA 672

Qy 138 LeuValPhe---AsnLeuLeuGlyLysAsnValThrArgAspAlaThrAspIle 156
         ||| ||| :::
Db   673 TTAACTTTTGCTACAGAAAACTAGTTCAAAAGTAAAAAGGATGGCTCCTCCTGCAGATATT 732

Qy 157 GluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsn 176
         ::: ||| ::::|| :::
Db   733 CGTGATGAGTGAACTGAGTTAACTGAACGAAAAGTAACAAAGTTAAACATATTGAAGGGAT 792

Qy 177 ValAspGluPheGlyAlaSerPheAsnLysLeuSerPheThrThrGlyLeuPheGly 196
         |||||| ||| :::|||||||||
Db   793 GGTTTTGAATTTACCTTAATACATTCCACGATGTAAATGGTAGGAAAAATTAATTATTCGGG 852

Qy 197 ---TrpGlyIleLysArgAlaLeuLysGlnIleLeuIleGluArgSerAsnLeuProLeu--- 213
         :::|| ||| :::
Db   853 CGTTCAGCTTTAAAACTGCATCCGGAAAATTAATTACTAAGAAAAATGTAAAACAAGTGGC 912

Qy 214 --AspIleGlyThrGluHisSer-------------ValSerArgLeuGlnHisIleThr 228
         :::::||||| |||||
Db   913 AGTGAGGTCCGAAAATGTTTATAACTTCCTAATTGTATTAACAGCTCTGCAA------- 963

Qy 229 SerSerTyrLysAspTyrMetAspThrGlnIleIleProAlaLeuProLysPheAlaLysArg 248
         ||| |||
Db   964 --------------AGTGATGAAGATGCAAAAGATGATTGTGGAAGCTAAACCAGGACATG 972

Qy 249 PheSerLeuMetValAlaGlnLeuLeuAlaThrValAlaGlyIleThrValAspThrPro 268
         ||| :::|||||||
Db   973 TTTCTTACTTTAACCATGCCGGAAAATTATTAGGCTTACAGATAATTGATTATATCTTCT 1032

Qy 269 TrpTyrLysGlyTrpThrTyrMetLysGluLeuLys---AsnPheMetValAsnArgValPheIle 287
         ||||||||| |||||||
Db 1033 ATTATGAAAGTGAACATTTAAATAAGGAAAAAAGAGGAAATTTAGAGTAAAC----ATCCTC 1086

Qy 288 ProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLeuGluLys 307
         ||||||| :::
Db 1087 CCTTACA----------CTTTCTATACTTTTTCTAAATCCTAAATTATGCAAAAGTTAAAGGA 1137

Qy 308 ValSerThrAspTrpAsnLeuAspValAsnLysIleGlyGlnThrValAspPhe 327
         ||| ||| :::
Db 1138 AGTGATGAAGATGCAAAAGATGATTGTGGAAGCTAAACCAGGACATGCCATTGATTGGGTTT 1197

Qy 328 PheAsnLysGluIleArgAspProSerLysAlaLeuLeuGluLysValSerAspAla 347
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Db 1198 GAAATTAGTAATGATTCA 1215

Qy 348 --------------LysAspLeuPheGluAsnLysIleGlyGlnThrValAspPheIleAsn 364
         |||||||
Db 1216 ATTACAGTATTAAAAGTATTAGAGGCTAAGCTAAAGACAA----AAT 1257

Qy 365 AsnGluIleArgAspProSerLysAlaLeuLeuIleLysValSerThrGlyAlaGluAsp 384
         ||| :::
Db 1258 TATCAAGTC------------GATAAGGATTCCTTATCGGAAGTTATTTATGCGATATGGAT 1308

Qy 385 ---------LeuPheGluAsnLysIleGlyGlnThrValAspPheIleAsnAsnGluIle 402
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Db 1309 AAATTATTGTGCCCAGATCAAATCTGGACAA----ATCTATTATACAAATAACATA 1359

Qy 403 ArgAspProSerLysAlaLeuLeuIleArgLysVal-------------- 413
         |||:::::|||||||
Db 1360 GTATTTCCAAATGAATATGTAAATTACTAAAAAATGAATTCACTAAAACTTTA 1419

Qy 414 --TyrThrGluAlaAspLeuPheGluAsnLysIleGlyGlnThrValAspPhe 432
         ||| :::
Db 1420 AGATATGAGGTAACACGGAATTTTTTATGGATTCTTCTACAGGAGAA------ATTGAC--- 1470

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Qy    433 IleAsnLysGluGluArgAspProSerLysAlaLeuIleArgLysValSerThrGluAla 452
          ::::||||||:::||    |||    :::    ::::||    :::::||
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Qy    453 AspAsnLeu 455
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Db   1531 GATGGGGTG 1539
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RESULT 37

US-08-471-044-31

Sequence 31, Application US/08471044

Patent No. 5840868

GENERAL INFORMATION:

APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Michael A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J

TITLE OF INVENTION: Pesticidal Proteins and Strains

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403

REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SQLv3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8689
TELEFAX: 919-541-8582

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 2612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS
LOCATION: 118..2484
OTHER INFORMATION: /note= "Native DNA sequence
encoding VIP3A(b) from AB424"

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US-08-471-044-31

Alignment Scores:
Pred. No.:              0.123
Score:                  96.50
Percent Similarity:     36.18%
Best Local Similarity:  20.28%
Query Match:            4.09%
DB:                     2

Length:        2612
Matches:       102
Conservative:  80
Mismatches:    202
Indels:        119
Gaps:          24
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US-09-807-459-2 (1-458) x US-08-471-044-31 (1-2612)

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Qy      4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
          :::|||    ||||||:::||    |||||||    ||:::
Db    235 ACGGATACAGGTGGTGATCTAACC--------------------------CTAGACGAA 267

Qy     24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
          :::    ::::||||||:::||    ::::||||::::||    ||:::
Db    268 ATTTTAAAGAATACAGACTACTAAAATGATATTTTCTGGTAAAATTGGAATGGGGTGAATGGA 327

Qy     44 AsnPheLeuGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
          :::    |||    |||    ||:::    |||    :::
Db    328 AGCTTAAAATGATCTTATCGCACAG--------------GGAAACTTAAATACAGAATTA 372

Qy     64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
          :::    ||    ||:::    |||    :::
Db    373 TCTAAGGAAAATATTAAAAAATTGCAAATCGAACAAAAATCAAGTTTTAAATGATGTTAATAAC 432

Qy     84 ProLeuGluAla-------------------------LysTyrGlnPro- 91
          ||||||    |||    |||
Db    433 AAAACTCGATCGGATAAAATACGAATCGTTCGGGTATATCCTACCTAAAAATTACCTCTATGTTG 492

Qy     92 ----------------------LeuThrLeuProAspProTyr-----Gln 99
          |||:::||    |||    |||
Db    493 AGTGATGTAATGAAACAAAAATTATGCGGTAAGTTCTGCAAATAGAAATACTTAAGTAAACAA 552

Qy    100 LeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnPro------AlaAsnSerThr 118
          :::||    :::    |||    ::::||    |||
Db    553 TTGCAAGAGATTTCTGATAAGTTGGATTATTAATATTAAATGTAAATTATTAAACTCTACA 612

Qy    119 GluLysArgPheTrpMetAspPheAspArgArgGlyLysAsn---HisSerTyrPheHisAsp 137
          |||    :::||    ||    :::    |||    :::
Db    613 CTTACTGAAAATTACACCTCGCGTATCAAAGGATTAAAATATGTGAAACGAAAAATTTGAGGAA 672

Qy    138 LeuValPhe---AsnLeuLeuGluLysAsnValThrArgAspAlaAsnSerAlaThrAsp 156
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Db    673 TTAACTTTTGCTACAGAAAACTAGTTCAAAAGTAAAAAAGGATGGCTCTCCTGCAGATATT 732

Qy    157 GluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsn 176
          :::    ||    :::||    :::    |||
Db    733 CGTGATCAGTTAACTGAGTTAACTGACTAGCCAAAAAGTGTAACAAAAAATGATGTGGAT 792

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Db    793 GGTTTTGAATTTTACCTTAATACATTCCACGATGTAAATGGTAGGAAATAATTTATTCGGG 852

Qy    197 --TrpIleLysSerArgGlyAlaLeuLysGlnIleIleIleArgSerAsnLeuProLeu----- 213
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Db    853 CGTTCAGCTTTAAAAACTGCATCGGAATTAAATTACTAAAGAAAAATGAAAACAAGTGGC 912

Qy    214 --AspIleGlyThrGluHisSer--------------ValSerArgLeuGlnHisIleThr 228
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Db    913 AGTGAGGTCGGAAAATGTTTATAACTTCCTAATTGTAATTAATTAACAGCTCGTCCAA----- 963

Qy    229 SerSerTyrArgLysAspTyrMetAspTyrMetAsnIleProAlaLeuProLysPheAlaLysArg 248
          :::    |||    |||    :::|||    |||||||||||
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Qy    249 PheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGlyValTyrValAspThrPro 268
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Qy    269 TrpTyrLysLysTrpTyrMetLysLeuLys---AsnPheMetValAsnArgValPheIle 287
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FILING DATE:
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PRIOR APPLICATION DATA:
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  FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/218,018
  FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/037,057
  FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Spruill, W. Murray
  REGISTRATION NUMBER: 32,943
  REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 919-541-8615
  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
  LENGTH: 2612 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
  NAME/KEY: CDS
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  OTHER INFORMATION: /note= "Native DNA sequence
  OTHER INFORMATION: encoding VIP3A(b) from AB424"
US-08-463-483A-31

Alignment Scores:
Pred. No.:              0.123
Score:                 96.50       Length:      2612
Percent Similarity:    36.18%      Matches:     102
Best Local Similarity: 20.28%      Conservative: 80
Query Match:            4.09%      Mismatches:  202
DB:                      2         Indels:      119
                                   Gaps:        24

US-09-807-459-2 (1-458) x US-08-463-483A-31 (1-2612)

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Qy     24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
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Db    268 ATTTTAAAGAATCACCAGCTACTAAAATGATAATTTCGTGTAAAATTGGATGGGTGAATGGA 327

Qy     44 AsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
          :::||||||:::|||
Db    328 AGCTTAAATGATCTTATCGCACAG---------------GGAAACTTAAATACAGAAATTA 372

Qy     64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
          :::|||:::|||
Db    373 TCTAAGGAAATAATTAAAAATTGCAAATGAACAAATCAAGTTTTAAAATGATGTTAATAAC 432

Qy     84 ProLeuGluAla---------------------------LysTyrGlnPro 91
          ||||||:::|||
Db    433 AAACTCGGATCGATAAATACGATCGCTTCGGGTATATCTACCTAAAATTACCTCTATGTTG 492

Qy     92 ----------------LeuThrLeuProAspProTyr----------Gln 99
          ||||:::|||
Db    493 AGTGATGTAATGAAACAAAATTATGCGTCTGCAAATGAAGTCTGCAAATAACTTAAGTAGAAACAA 552

Qy    100 LeuGluLeuAlaPheIleLeuPheLysGluSerAspAlaAsnPro---AlaAsnSerThr 118
          |||:::||
Db    553 TTGCAAGAGAGATTTCTGATAAGTTGGATATTATTAATGTACTTAATAACTCTACA 612

Qy    119 GluLysArgPheTrpMetArgPheArgArgGlyLysAsn---HisSerTyrPheHisAsp 137
          :::::|||
```

GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
  ADDRESSEE: CIBA-GEIGY Corporation
  STREET: 7 Skyline Drive
  CITY: Hawthorne
  STATE: NY
  COUNTRY: USA
  ZIP: 10532
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/463,483A

RESULT 38
US-08-463-483A-31
Sequence 31, Application US/0846483A
Patent No. 5849870

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Qy   1033 ATTATGAAATGAACATTTAAATAAGGAAAAGAGGAATTTAGAGTAAAC-----ATCCTC 1086
              |||||            |||||||
Db   1087 CCTACA--------CTTTCTAATACTTTTCTTAATCCTAATTATATGCAAAAGTTAAAGGA 1137

Qy    288 ProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLys 307
              ||||||    :::
Db    308 ValSerThrAspThrLysAspAspLeuProLysProAsnLysLysIleGlyGlnThrValAspPhe 327
              ||| |||

Qy   1138 AGTGATGAAGATGCAAAGATGCGATTGTGTGAAGCTAAACCAGACATGCATTGATTGGGTTT 1197
              |||  |||
Db    328 PheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAla 347
              :::|||||||||||||||:::

Qy   1198 --------------------GAAATTAGTAATGATTCA 1215
              :::|||||||||||||||:::
Db    348 ------LysAspLeuPheGluGlnAsnLysIleGlyGlnThrValAspPheIleAsn 364
              :::|||

Qy   1216 ATTACAGTATATAAAAGTATATCGAGGCGTAAGCTAAAACAA------AAT 1257
              :::|||
Db    365 AsnGluIleArgAspProSerLysAlaLeuIleLeuArgLysValSerThrGlyAlaGluAsp 384
              :::|||

Qy   1258 TATCAAGTC----------GATAAGGAGTTCCTTATCGGAAGTTATTATTTATGGGGATATGGAT 1308
              :::|||
Db    385 ------LeuPheGluAsnLysIleGlyGlnThrValAspPheIleAspAsnGluIle 402
              :::|||

Qy   1309 AAATTAATTGTGCCCAGATCACAATCTGGACAA-------ATCTATTATACAAATAACATA 1359
              :::  |||
Db    403 ArgAspProSerLysAlaLeuIleLeuArgLysVal------------------- 413

Qy   1360 GTATTTCCAAATGAATATGTAATTACTAAAATTGAATTCACTAAAAAAATGAAAACTTTA 1419
              :::||||||||::||
Db    414 ---TyrThrGluAlaAspAspLeuPheGluAsnLysIleGlyGlnThrValAspPhe 432
              :::  |||

Qy   1420 AGATAGTGAGGTAACACGGAATTTTATGATTCTTCTACAGGAGAA---ATTGAC-- 1470
              |||:::
Db    433 IleAsnLysGluIleArgAspProSerLysAlaLeuIleLeuArgLysValSerThrGlyAla 452

Qy   1471 TTAAATAAGAAAAAAGTAGAATCAAGTGAACGGGAGTATAGAACGTTAAGTGCTAATGAT 1530
              |||||||||::|||
Db    453 AspAsnLeu 455
              :::|||

Qy   1531 GATGGGGTG 1539
              ||| :::
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Db  613  CTTACTGAAATTACACCTGCCGTATCCAAAGGATTAAATATGTGAACGAAAAATTTGAGGAA  672

Qy  138  LeuValPhe---AsnLeuLeuGlyLysAsnValThrArgAspAlaAlaAspAlaThrAspIle  156
              |||                                                  |||
Db  673  TTAACTTTTGCTACAGAAACTAGTTCAAAAGTAAAAAGGATGGCTCTCCTGCAGATATT  732

Qy  157  GluAsnPheAlaSerArgTyrLeuTyrLeuTyrTyrLysThrThrTyrThrAsn  176
                ::;                                   |||
Db  733  CGTGATGAGTTAACTGAGTTAACTAGCGAAAAGTGTAACAAAAAATGATGTGGAT  792

Qy  177  ValAlaSpGluPheGlyTyrAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGly  196
              |||||||
Db  793  GGTTTTGAATTTTACCTTTAATACATTCCACGATGTAAGTGTAGGAAAATAATTTATTCGGG  852

Qy  197  ---TrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeu-----  213
                |||  :::    :::
Db  853  CGTTCAGCTTTAAAAACTGCATCCGAATTAATTAACTACTAAAGAAAATGTGAAAACAAGTGGC  912

Qy  214  --AspIleGlyThrGluHisSer------  228
                |||                ||||||
Db  913  AGTGAGGTCGGAAATGTTTATAACTTCCTTAATTGTATTATAACAGCTCTGCAA-------  963

Qy  229  SerSerTyrLysAspTyrMetAspThrGlnIleProLysAlaLeuProLysPheAlaLysAsrg  248
                                                              |||||||
Db  964  --------GCAAAAGCT  972

Qy  249  PheSerLeuMetValValGlnAsnLeuLeuAlaThrValAlaAlaGlyThrTyrValAspThrPro  268
              |||    :::                            |||
Db  973  TTTCTTACTTTAACACCATGCCGAAAATTATTAGGCTTAGCCAGATATTGATTATATACTTCT  1032

Qy  269  TrpTyrLysLysTrpTyrMetLysLysLeuLys--AsnPheMetValAlaAsnArgValPheIle  287
              ||||||                              ||||||
Db  1033 ATTATGAATGAACATTTAAATAAGGAAAAAAGAGAGAGAATTTAGAGTAAAC-----ATCCTC  1086

Qy  288  ProThrLysLysPhePheAsnLysGluIleArgGluProSerLeuLysSerGluLys  307
                ::;
Db  1087 CCTACA------CTTTCTAATACTTTTTCTAATCCTAATTATGCAAAAAGTAATATATCTCT  1137

Qy  308  ValSerThrAspThrLysAspLeuPheGluAsnLysLysIleGlyInGlyThrValAspPhe  327
              |||    :::                            |||
Db  1138 AGTGATGAAGATCCAAAAGATGATGTGGGAAGCTAAACCAGGACACATGCATTGATTGGGTTT  1197

Qy  328  PheAsnLysGluIleArgAspProSerLysAlaLeuLeuLysSerValSerArgAsnAspAla  347
                                                      |||||||
Db  1198 ------GAAATTACTAATGCATTCA  1215

Qy  348  ---LysAspLeuPheGluAsnLysIleGlyInGlyThrValAspPheIleAsn  364
                |||    :::                            |||
Db  1216 ATTACAGTATTAAAAGTATATGAGGCTAAGCTAAAACAA-------AAT  1257

Qy  365  AsnGluIleArgAspProSerLysAlaLeuLeuIleArgLysSerValSerThrGlyValAlaGlyAsp  384
              |||    :::                            |||
Db  1258 TATCAAGTC------GATAAGGATTCCTTATCGGAAGTATATTATTATGGCGATATGGAT  1308

Qy  385  ---LeuPheGluAsnLysIleGlyInGlyThrValAspPheIleAsnAsnGluIle  402
                |||    :::                            |||
Db  1309 AAATTATTGTGCCAGATCAATCTGGACAA-------ATCTATTATACAAAATAACATA  1359

Qy  403  ArgAspProSerLysAlaLeuLeuIleArgLysSerVal-----  413
                |||    :::                    |||
Db  1360 GTATTTCCAAATGAATATGTAATTACTAAAAAATGAAAAACTTTA  1419

Qy  414  --TyrThrGluAlaAspLeuPheGluAsnLysIleGlyInGlyThrValAspPhe  432
                |||                            |||
Db  1420 AGATATGAGGTAACAGCGAATTTTTATGATTCTTCTCACAGGAGAA-----ATTGAC---  1470

Qy  433  IleAsnLysGluIleArgAspProSerLysAlaLeuLeuIleArgLysSerValSerThrGluAla  452
              ::|||||;  ::                          |||
Db  1471 TTAAATAAGACAAAAAGTAGAATCAAGTGAAGCGGAGTATAGAACGTTAGTGCTTAATGAT  1530

Qy  453  AspAsnLeu  455
              :::
Db  1531 GATGGGGTG  1539
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Alignment Scores:
Pred. No.:   0.123
Score: 96.50
Percent Similarity: 36.18%
Best Local Similarity: 20.28%

Length: 2612
Matches: 102
Conservative: 80
Mismatches: 202

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Query Match:         4.09%          Indels:     119
DB:                  2              Gaps:       24

US-09-807-459-2 (1-458) x US-08-471-046A-31 (1-2612)

Qy      4  SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
           :::||:|:|||                                   :::||
Db    235  ACGGATACAGGTGGTGATCTAACC----------------------------CTAGACGAA 267

Qy     24  AlaAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspThrLeuSerAlaValSerAsp 43
           ::|||||||:::||                                :||||:::|
Db    268  ATTTTAAAGAATCAGAGCTACTAAATGATATTTCTCGTAAATTGGATGGGTGAATGGA 327

Qy     44  AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
           :::                      |||                  |||
Db    328  AGCTTAAATGATCTTATCGCACAG---------------GGAAACTTAAATACAGAATTA 372

Qy     64  SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
           ::|                     |||||                      |||
Db    373  TCTTAAGGAAATATTAAAAAATTGCAAATGAACAAAATGAGTTTTAAAAATGAGTTAATAAC 432

Qy     84  ProLeuGluAla--------------LysTyrGlnPro 91
           |||||:|:|||                   |||
Db    433  AAACTCGATGCGATAAATACGATGCTTCGGGTATATCTCCTAAAATTACCTCTATGTTG 492

Qy     92  ----------------LeuThrLeuProAspProTyr-----------Gln 99
                            ||||                            |||
Db    493  AGTGATGTAATGACAAACAAAAATTATGCGCTAAGTCTCGCAAATAGAAATACTTAAGTACAACAA 552

Qy    100  LeuGluIleAlaLeuPheLeuGluGlySerAspAlaAsnPro-------AlaAsnSerThr 118
           ::                      |||                      |||
Db    553  TTGCAAGAGATTTTCTGATAAGTTGGATAATTATTAATGTAAATGTACTTATTATTAACTCTACA 612

Qy    119  GluLysArgPheTrpMetArgPheArgArgGlyLysAsn---HisSerTyrPheHisAsp 137
           |||||||                      :||:              :::
Db    613  CTTACTGAAAATTACACCTGCGTATCAAAAGGATTAAATATGTGAACGAAAAATTTGAGGAA 672

Qy    138  LeuValPhe---AsnLeuLeuGlyLysAsnValThrArgAspAlaProAlaThrAspIle 156
           |||          |||             |||            |||
Db    673  TTAACTTTTGCTACAGAAACTAGTTCAAAAGGTAAAAAAGGACCTCCTCCGCAGATATT 732

Qy    157  GluAsnPheAlaSerArgTyrTyrLysThrThrGlyTyrTyrLysThrThrGlyTyrThrAsn 176
           :::                      ||||            |||
Db    733  CGTGATGAGTTAACTGAGTTAACTGAACAGTGTAACAAAAGTGATGTGGAT 792

Qy    177  ValAspGluPheGlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGly 196
           ||||||||                      |||||||||
Db    793  GGTTTTGAATTTACCTTAATACATTCCACGATGTAAATGGTAGGAAAATAAATTTATTCGGG 852

Qy    197  ---TrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeu---- 213
              |||||||              |||             ::|
Db    853  CGTTCAGCTTTAAAAACTGCATCGGAATTAATTACTAAAGAAAAATGTAAACAAGTGC 912

Qy    214  ---AspIleGlyThrGluHisSer--------ValSerArgLeuGlnHisIleThr 228
              |||||||||                   ||:
Db    913  AGTGAGGTCGGAAAGTGTTATAACTTCCTAATTGTATTAAACAGCTCTCCAA---- 963

Qy    229  SerSerTyrGlyLysAspTyrMetAspThrGlnIleIleProAlaLeuProLysArg 248
           |||||:|                   |||||||
Db    964  TTTCTTACTTTAACACCATGCCGAAAAATTATTAGGCTTAGCAGATATTATACTTCT 1032

Qy    249  PheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrPro 268
           |||  :::                      |||             |||
Db    973  TTTCTTACTTTAACACCATGCCGAAAAATTATTAGGCTTAGCAGATATTATACTTCT 1032

Qy    269  TrpTyrLysLysTrpTyrMetLysGlyLeuLys----AsnPheMetValAsnArgValPheIle 287
           |||                      :::           |||
Db   1033  ATTATGAATGAACATTTAAATAAGGAAAAAAGGAATTTAGACTAAAC-----ATCCTC 1086

Qy    288  ProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLys 307
           |||||||                      |||             |||
Db   1087  CCTACA------CTTTCTAATACTTTTTCTAATCCTAATTATATGCAAAAGTTAAAGGA 1137
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Qy    308  ValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe 327
           :::                      |||             :::
Db   1138  AGTGATGAAGAAGATGCAAAAGATGAATTGGAAGGCTAAAACCAGGACAATGCATTGGGTTT 1197

Qy    328  PheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAla 347
           |||             :::                      |||
Db   1198  ----------------LysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe 364
           
Db   1216  ATTACAGTATTAAAGTATATGAGGGCTAAGCTAAAACA---------------------- 1257

Qy    365  AsnGluIleArgAspProSerLysAlaLeuLeuIleArgLysValSerThrGlyAlaGluAsp 384
           |||             :::                      |||
Db   1258  TATCAAGTC----------GATAAGGATTCCTTATCGGAAGTTATTTATGGGATATGGAT 1308

Qy    385  ------LeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnGluIle 402
                 |||             :::
Db   1309  AAATTATTGTGCCCAGATCAATCTGGACAA--------AATCTATTATACAAATAACATA 1359

Qy    403  ArgAspProSerLysAlaLeuLeuIleArgLysVal--------------------- 413
           |||             :::
Db   1360  GTATTTCCAAAATGAATATGTAATTACTAAAATTGATTTCACTAAAAATGAAAACTTTA 1419

Qy    414  ---TyrThrGluAlaAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe 432
              |||             :::                      |||
Db   1420  AGATGATGAGGTAACAGCGAATTTTTATGATTCTTCTACAGGAGAA-----ATTGAC-- 1470

Qy    433  IleAsnLysGluIleArgAspProSerLysAlaLeuLeuIleArgLysValSerThrGluAla 452
           |||:::::||                      :::||
Db   1471  TTAAATAAGAAAAAGTAGAATCAAGTGAAGCGGAGTATAGAACGTTAAGTGCTAAATGAT 1530

Qy    453  AspAsnLeu 455
           |||
Db   1531  GATGGGGTG 1539
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RESULT 40
US-08-470-566B-31
; Sequence 31, Application US/08470566B
; Patent No. 5872212
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kisty
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
   ADDRESSEE: 5872212artis Corporation
   STREET: 3054 Cornwallis Road
   CITY: Research Triangle Park
   STATE: NC
   COUNTRY: USA
   ZIP: 27709
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/470,566B
   FILING DATE: 06-JUN-1995
   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 08/463,483
   FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 08/314,594
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FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 08/218,018
   FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 08/037,057
   FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
   NAME: Meigs, J. Timothy
   REGISTRATION NUMBER: 38, 241
   REFERENCE/DOCKET NUMBER: CGC1695/C1P3/DIV4 - SQLv4
TELECOMMUNICATION INFORMATION:
   TELEPHONE: 919-541-8689
   TELEFAX: 919-541-8587
INFORMATION FOR SEQ ID NO: 31:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 2612 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
   MOLECULE TYPE: DNA (genomic)
   HYPOTHETICAL: NO
   FEATURE:
      NAME/KEY: CDS
      LOCATION: 118..2484
      OTHER INFORMATION: /note- "Native DNA sequence
         encoding VIP3A(b) from AB424"
US-08-470-566B-31

Alignment Scores:
   Pred. No.:                0.123
   Score:                    96.50         Length:         2612
   Percent Similarity:       36.18%        Matches:         102
   Best Local Similarity:    20.28%        Conservative:     80
   Query Match:              4.098         Mismatches:      202
                                           Indels:          119
                                           Gaps:             24

US-09-807-459-2 (1-458) x US-08-470-566B-31 (1-2612)

Qy    4  SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer   23
Db  235  ACGGATACAGGTGGTGATCTAACC------------------CTAGACGAA           267

Qy   24  AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerLeuAlaValSerAsp  43
Db  268  ATTTTAAGAAGAATCAGCACCTACTAAATGATATATTCTGTGTAAATTGGATGGGGAATGGA  327

Qy   44  AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal   63
Db  328  AGTTAAATGATCTTATCGCACAG-----GGAAACTTAAATACAGAATTA             372

Qy   64  SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr   83
Db  373  TCTAAGGAAATATTAAAAATTGCAAATGAACAAAAATCAAGTTTTAAATGGTTAATAAC    432

Qy   84  ProLeuGluAla---------LysTyrGlnPro                              91
Db  433  AAACTCGATGGCGATAAAAATACGAGCCTTCGGGTATCATCTACCTAAAATTACCTCTATGTG  492

Qy   92  -----------LeuThrLeuProAspProTyr-----Gln                      99
Db  493  AGTGATGTAATGAAACAAAAATATGCGCTAAGTCTGCAAATAGAATACTTAAGTAAACAA   552

Qy  100  LeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnPro---AlaAsnSerThr  118
Db  553  TTGCAAGAGAATTTCTGATAAGTTGGATATATTAATGTAAAGTGTACTTATTAACCTCACA  612

Qy  119  GluLysArgPheTrpMetArgArgArgGlyLysAsn---HisSerTyrPheHisAsp    137
Db  613  CTTACTGAAATTACACCTGCGTATCAAAGGGATTTAAAATATGTGAACGAAAAATTTGAGGAA 672

Qy  138  LeuValPhe---AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIle  156
Db  673  TTAACTTTTGCTACAGAAACTAGTTCAAAAGTAAAAAAGGATGGCGTCTCGTCAGATATT  732

Qy  157  GluAspPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsn  176
Db  733  CGTGATGAGTTAACTGAGTTAACTAGACGAAAAGTGTAACAAAAAATGATGTGGAT      792

Qy  177  ValAspGluPheGlyAlaSerPheAsnLysLeuSerPheThrThrGlyLeuPheGly     196
Db  793  GGTTTTGAAATTTTACCTTAATACATTCCACGAGTGTAAATGGTTAGGAAAATAATTATTCGGG 852

Qy  197  ---TrpGlyIleLysArgAlaLeuLysGlnIleIleIleArgSerAsnLeuProLeu--- 213
Db  853  CGTTCAGCTTTAAAAACTGCATCGGAATTAAATTACTTAAAGAAAAGTGAAAACAAGTGGC  912

Qy  214  ---AspIleGlyThrGluHisSer---------ValSerArgLeuGlnHisIleIleThr 228
Db  913  AGTGAGGTCGGAAATGTTTATAACTTCCTAATTGTATTAAACAGCTCTGCAA          963

Qy  229  SerSerTyrLysAspTyrMetAspThrGlnIleIleProAlaLeuProLysPheArg    248
Db  964  --------------------GCAAAAGCT                                 972

Qy  249  PheSerLeuMetValValGlnArgLeuLeuAlaAlaThrValAlaLaGlyTyrValAspThrPro 268
Db  973  TTTCTTAACTTTAACACCATGCCGAAAAATTATTAGGCTGACAGATATTATACTTCT     1032

Qy  269  TrpTyrLysLysTrpTyrMetLysLysLeuLys---AsnPheMetValAsnArgValPheIle 287
Db 1033  ATTATGAAATGAACATTTAAATAAAGGAAAAAGAGGAATTTAGAGTAAAC---ATCCTC  1086

Qy  288  ProThrPheLysLysProPheAsnLysGluArgAsnGlyIleGlyGlyThrValAspLys  307
Db 1087  CCTACA----------CTTTCTAATACTTTTTCTAATCCTAATTATGCGAAAAGTTAAAGGA 1137

Qy  308  ValSerThrAspThrHrLysAspLeuPheGluAsnLysLysIleGlyGlnGlyThrValAspPhe 327
Db 1138  AGTGATGAAGAGATGCAAAAGATGTGTGGAAGGCTAAACCAGACATGCCATTGAGTTGGGTTT 1197

Qy  328  PheSerLysGluIleArgAspProSerLysAlaLysValValSerSerAsnAspAla    347
Db 1198  ---------------------GAAATTAGTAATTGATTCA                      1215

Qy  348  ------LysAspLeuPheGluAsnLysLysIleGlyGlnGlyThrValAspPheIleGlyIle 364
Db 1216  ATTACAGTATATTAAAAATGATATGCAGGCTAAAGCTAAGCTAAAGCAAAATGATAACATA  1257

Qy  365  AsnGluIleArgAspProSerLysAlaLeuLeuIleLeuArgGlyValAlaGluAsp    384
Db 1258  TATCAAGTC----------GATAAGGAAAATTCCTTATCCGGAAGTTATTTATGGGGATATGGAT 1308

Qy  385  ------LeuPheGluAsnLysLysIleGlyGlnGlyThrValAspPheIleGlyIle     402
Db 1309  AAATTAATTGTGCCCAGATCAATCATGTCTGGACAA---                       1359

Qy  403  ArgAspProSerLysAlaLeuLeuIleLeuArgLysVal---                   413
Db 1360  GTATTTCCAAATGAATAGTAATTACTAAAAATGAAAAACTTTA                  1419

Qy  414  ---TyrThrGluAlaAspSerLeuPheGluAsnLysLysIleGlyGlnGlyThrValAspPhe 432
Db 1420  AGATATGAGGTAACACGCGAATTTTATGATTCTTCTACAGGAGAA---             1470

Qy  433  IleAsnLysGluIleArgAspProSerLysAlaLeuLeuIleLeuArgLysValSerThrGluAla 452
Db 1471  TTAAATAAGAAAAAAGTAGAACGTAGAAGTAGGAGTATAGAAACGTAAGTCCTAATGAT   1530

Qy  453  AspAspAsnLeu                                                 455
Db 1531  GATGGGGTG                                                    1539

Search completed: October 19, 2002, 09:03:57
Job time : 115 secs
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